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OM protein - protein search, using sw model

Run on: October 31, 2003, 13:55:32 ; Search time 83 Seconds

(without alignments)  
128.129 Million cell updates/sec

Title: US-09-872-852-2

Perfect score: 367

Sequence: 1 MRLHLLPALLFLFLVPVG.....KEEQIGKSTRGKCRKK 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	100.0	67	20	AAU07244
2	367	100.0	67	21	AA10602
3	367	100.0	67	23	AA017768
4	367	100.0	67	23	AAU91016
5	367	100.0	67	23	AAU91036
6	367	100.0	67	23	AAU09707
7	357	97.3	65	20	AAU07243
8	250	68.1	45	21	AA10600
9	250	68.1	45	23	AA017767

10	250	68.1	45	23	AAU09709	Human beta-defensi
11	230	62.7	41	23	AAU09708	Human beta-defensi
12	225	61.3	40	23	AA017766	Human beta-defensi
13	177	48.2	31	23	AA017765	Human beta-defensi
14	177	48.2	31	23	AA049572	Human beta-defensi
15	177	48.2	31	23	AA049576	Human beta-defensi
16	173	47.1	32	21	AA010621	Human SAP-3 N-term
17	163	44.4	51	20	AAU12039	Human 5' EST seque
18	148	40.3	27	23	AA017773	Human beta-defensi
19	148	40.3	27	23	AA017781	Human beta-defensi
20	136	37.1	24	23	AA017774	Transplant media a
21	135	36.8	64	23	AAU91048	Amino acid sequenc
22	133	36.2	64	20	AAW81071	Transplant media a
23	133	36.2	64	23	AAU91049	Mouse beta-defensi
24	121.5	33.1	63	22	AAE02126	Human beta-defensi
25	118	32.2	22	23	AA017772	Human beta-defensi
26	113	30.8	64	17	AA086894	Prepro-LAP. Bos t
27	113	30.8	64	23	AAU90965	Transplant media a
28	112	30.5	19	23	AAU01770	Human beta-defensi
29	111	30.2	64	13	AA024332	Tracheal antimicro
30	111	30.2	64	16	AA066205	Bovine tracheal an
31	111	30.2	64	16	AA066204	Bovine tracheal an
32	111	30.2	64	19	AA065966	Mouse zamp3 (Defb5
33	107.5	29.3	63	22	AAE02122	Prepro-LAP #2. Sy
34	107	29.2	65	17	AA086896	Transplant media a
35	105	28.6	64	23	AAU91052	Transplant media a
36	100	27.2	64	23	AAU91051	Human beta-defensi
37	93	25.3	17	23	AA017771	Human beta-defensi
38	93	25.3	17	23	AA017780	Mouse beta-defensi
39	90.5	24.7	63	22	AAE02127	Bovine neutrophil
40	89	24.3	42	15	AA063515	Transplant media a
41	89	24.3	42	23	AAU91028	Mouse beta-defensi
42	85	23.2	69	19	AAW53857	Human zamp2 protei
43	85	23.2	69	22	AAE02125	Amino acid sequenc
44	78	21.3	80	22	AA084568	Amino acid sequenc
45	76	20.7	80	22	AA084567	Amino acid sequenc

#### ALIGNMENTS

RESULT 1  
AAU07244  
ID AAU07244 standard; Protein; 67 AA.

AC AAU07244;

XX 06-JUL-1999 (first entry)

DT Beta-defensin family member zamp1.

DE Human; zamp1; beta-defensin; bacterium; fungus; inflammation;  
KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;  
KW antibody; ion flux; cytotoxic activity; mammalian cell.

OS Homo sapiens.

PN WO9913080-A1.

XX 18-MAR-1999.

XX 10-SEP-1998; 98WO-US19222.

XX 05-NOV-1997; 97US-0964687.

XX 10-SEP-1997; 97US-0058335.

XX 10-SEP-1997; 97US-0926529.

XX 05-NOV-1997; 97US-0064294.

XX (ZYMO ) ZYMOGENETICS INC.

XX Adler D, Baidur N, Beigel S, Holloway JL;

XX WPI; 1999-215064/18.

DR N-PSDB; AAX29986.  
 XX New zampl polypeptide and polynucleotide, human beta-defensins -  
 PT useful as diagnostic reagents and for treatment of microbial  
 PT infections, and AIDS  
 XX Claim 1; Page 73; 79pp; English.  
 XX This sequence represents the human zampl protein which is a member of the  
 CC beta-defensin protein family. Zampl protein is useful as a pharmaceutical  
 CC composition, useful for treatment of e.g. bacterial, fungal and viral  
 CC infections. They are also useful pro-inflammators, for treating chronic  
 CC tissue damage, and for stimulating the immune response, for treatment of  
 CC AIDS or chemotherapy patients. Zampl polypeptides and antibodies are  
 CC useful for studying activity of the melanocortin family, studying ion  
 CC flux in cell culture, and studying cytotoxic activity against mammalian  
 CC cells in culture, by incubation with the cells. Zampl polypeptides are  
 CC especially useful for studying epithelial defensin induction in cell  
 CC culture when exposed to pathogenic stimuli.  
 XX Sequence 67 AA;  
 SQ  
 Query Match 100.0%; Score 367; DB 20; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-37;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRHYLLFALLFLFLVPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKCTRGR 60  
 DB 1 MRHYLLFALLFLFLVPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKCTRGR 60  
 QY 61 KCCRKK 67  
 DB 61 KCCRKK 67  
 RESULT 2  
 ID AAB10602 standard; Protein; 67 AA.  
 AC AAB10602;  
 XX 08-JAN-2001 (first entry)  
 DE Human SAP-3 pre-protein.  
 XX SAP-2; SAP-3; human; antibiotic; antibacterial; antifungal; antiviral;  
 KW treatment; microbial infection; wound dressing; diagnostic reagent.  
 XX Homo sapiens.  
 OS WO200046245-A2.  
 FN 10-AUG-2000.  
 PD 01-FEB-2000; 2000WO-EP00776.  
 PF 01-FEB-1999; 99DE-1005128.  
 PR 08-OCT-1999; 99DE-1049436.  
 XX (SCHD ) SCHERING AG.  
 PA Christophers E, Harder J, Schroeder J;  
 PI WPI; 2000-514948/46.  
 DR N-PSDB; AAX71755.  
 XX New human antibiotic peptides, useful for treating microbial  
 PT infections, particularly when incorporated in wound dressings, also  
 PT related nucleic acid -  
 XX Claim 4; Page 39; 41pp; German.  
 PS This invention describes the novel active, mature human proteins (I)  
 CC

CC SAP-2 and SAP-3 which have antibiotic, antibacterial, antifungal and  
 CC antiviral activity. (I), and their precursors, are useful for treating  
 CC or preventing microbial infections (caused by bacteria, fungi or  
 CC viruses), particularly where they (or human cells expressing them) are  
 CC included in wound dressings, and to produce specific antibodies (Ab) or  
 CC their fragments. Ab are used as diagnostic reagents, e.g. to detect a  
 CC deficiency of (I) or the presence of a (I) variant. This sequence  
 CC represents the human SAP-3 protein described in the method of the  
 CC invention.  
 XX Sequence 67 AA;  
 SQ  
 Query Match 100.0%; Score 367; DB 21; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-37;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRHYLLFALLFLFLVPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKCTRGR 60  
 DB 1 MRHYLLFALLFLFLVPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKCTRGR 60  
 QY 61 KCCRKK 67  
 DB 61 KCCRKK 67  
 RESULT 3  
 ID AAO17768 standard; protein; 67 AA.  
 XX AAO17768;  
 AC AAO17768;  
 XX 30-AUG-2002 (first entry)  
 DE Human beta-defensin-3 derivative #3.  
 XX Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;  
 KW respiratory system; cystic fibrosis; inflammation; urogenital tract;  
 KM antibacterial; fungicide; cytostatic; antiinflammatory; antiulcer;  
 KW gastrointestinal tract; septicaemia; apoptosis induction; cancer.  
 XX Homo sapiens.  
 OS WO200240512-A2.  
 FN 23-MAY-2002.  
 PD 14-NOV-2001; 2001WO-EP13174.  
 PF 14-NOV-2000; 2000DE-1056365.  
 PR 30-MAR-2001; 2001DE-1016220.  
 XX (IPFP-) IPF PHARM GMBH.  
 PA Forssmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;  
 PI Maegert H;  
 XX WPI; 2002-435959/46.  
 DR New human beta-defensin 3, useful for treating or preventing microbial  
 PT infection and tumors, also related nucleic acid -  
 XX Claim 2; Page 23; 36pp; German.  
 XX The present invention relates to human beta-defensin-3 (hBD-3) and its  
 CC derivatives. The peptide, its coding sequence and vectors containing the  
 CC coding sequence are useful in (gene) therapy and diagnosis, especially  
 CC for preventing or treating a wide range of microbial infections  
 CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the  
 CC respiratory tract, especially in cases of cystic fibrosis, and  
 CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal  
 CC and urogenital tracts, sepsis and yeast infections), and for inducing  
 CC apoptosis for treating malignant melanoma and tumours. The present  
 CC sequence is a derivative of human BD-3.

Query Match 100.0%; Score 367; DB 23; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.5e-37; Mismatches 0; Indels 0; Gaps 0;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFLVPPVPGHGIINTLQKYCYVRGRCVLSCLPKKEQIGKCTRGR 60  
DB 1 MRIHYLLFALLFLFLVPPVPGHGIINTLQKYCYVRGRCVLSCLPKKEQIGKCTRGR 60  
QY 61 KCCRKK 67  
DB 61 KCCRKK 67

RESULT 6  
AAU09707  
ID AAU09707 standard; Protein; 67 AA.  
AC AAU09707;  
XX  
XX  
XX 26-MAR-2002 (first entry)  
DT  
DE Human beta-defensin-3 (HBD-3).  
XX  
XX Human; antimicrobial peptide; human beta-defensin-3; HBD-3;  
KW microbial growth; microbial infection; pulmonary infection.  
KW  
XX Homo sapiens.  
OS  
XX WO200192309-A2.  
PN  
XX 06-DEC-2001.  
PD  
XX 01-JUN-2001; 2001WO-US18057.  
PF  
XX 01-JUN-2000; 2000US-208792P.  
PR  
XX (IOWA) UNIV IOWA RES FOUND.  
PA  
XX McCray PB, Tack B, Jia HP, Schutte BC;  
PI  
XX WPI; 2002-106302/14.  
DR  
XX N-PSDB; AAS14407.  
XX  
XX New human beta-defensin 3 peptides and nucleic acids encoding peptides,  
PT useful for treating or preventing microbial growth or infection, or in  
PT gene therapy -  
XX  
XX Claim 1; Page 96; 110pp; English.  
PS  
XX The present invention relates to the isolation of a novel antimicrobial  
CC peptide, human beta-defensin-3 (HBD-3). Also described is a method of  
CC inhibiting growth of a microbe by introducing into a host or environment  
CC the antimicrobial peptide of the invention. The peptide is useful for  
CC treating or preventing microbial growth or infections, e.g. pulmonary  
CC infections when administered by inhalation. The peptide can be applied  
CC on a work surface or a surgical instrument for the prevention and/or  
CC suppression of microbial growth. The present sequence represents  
CC HBD-3.  
XX  
SQ Sequence 67 AA;  
Query Match 100.0%; Score 367; DB 23; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.5e-37;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFLVPPVPGHGIINTLQKYCYVRGRCVLSCLPKKEQIGKCTRGR 60  
DB 1 MRIHYLLFALLFLFLVPPVPGHGIINTLQKYCYVRGRCVLSCLPKKEQIGKCTRGR 60  
QY 61 KCCRKK 67  
DB 61 KCCRKK 67

RESULT 7  
AAU07243  
ID AAU07243 standard; Protein; 65 AA.  
AC AAU07243;  
XX  
XX 06-JUL-1999 (first entry)  
DT  
DE Beta-defensin family member zamp1.  
XX  
XX Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;  
KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;  
KW antibody; ion flux; cytotoxic activity; mammalian cell.  
XX  
XX Homo sapiens.  
OS  
XX WO9913080-A1.  
PN  
XX 18-MAR-1999.  
PD  
XX 10-SEP-1998; 98WO-US19222.  
PF  
XX 05-NOV-1997; 97US-0964687.  
PR  
XX 10-SEP-1997; 97US-0058335.  
PR  
XX 10-SEP-1997; 97US-0926529.  
PR  
XX 05-NOV-1997; 97US-0064294.  
XX  
XX (ZYMO) ZYMOGENETICS INC.  
XX  
XX Adler D, Baidur N, Beigel S, Holloway JL;  
PI  
XX WPI; 1999-215064/18.  
DR  
XX N-PSDB; AAX29985.  
XX  
XX New zamp1 polypeptide and polynucleotide, human beta-defensins -  
PT useful as diagnostic reagents and for treatment of microbial  
PT infections, and AIDS  
XX  
XX Claim 1; Page 70; 79pp; English.  
PS  
XX This sequence represents the human zamp1 protein which is a member of the  
CC beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical  
CC composition, useful for treatment of e.g. bacterial, fungal and viral  
CC infections. They are also useful pro-inflammators, for treating chronic  
CC tissue damage, and for stimulating the immune response, for treatment of  
CC AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are  
CC useful for studying activity of the melanocortin family, studying ion  
CC flux in cell culture, and studying cytotoxic activity against mammalian  
CC cells in culture, by incubation with the cells. Zamp1 polypeptides are  
CC especially useful for studying epithelial defensin induction in cell  
CC culture when exposed to pathogenic stimuli.  
XX  
SQ Sequence 65 AA;  
Query Match 97.3%; Score 357; DB 20; Length 65;  
Best Local Similarity 100.0%; Pred. No. 2.5e-36;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFLVPPVPGHGIINTLQKYCYVRGRCVLSCLPKKEQIGKCTRGR 60  
DB 1 MRIHYLLFALLFLFLVPPVPGHGIINTLQKYCYVRGRCVLSCLPKKEQIGKCTRGR 60  
QY 61 KCCR 65  
DB 61 KCCR 65

RESULT 8  
AAB10600  
ID AAB10600 standard; Protein; 45 AA.  
AC AAB10600;  
XX

DT 08-JAN-2001 (first entry)  
 XX Human SAP-3 mature protein.  
 DE  
 XX SAP-2; SAP-3; human; antibiotic; antibacterial; antifungal; antiviral;  
 KW treatment; microbial infection; wound dressing; diagnostic reagent.  
 XX  
 OS Homo sapiens.  
 XX WO200046245-A2.  
 PN  
 XX 10-AUG-2000.  
 PD  
 XX  
 PF 01-FEB-2000; 2000WO-EP00776.  
 XX  
 XX 01-FEB-1999; 99DE-1005128.  
 PR  
 PR 08-OCT-1999; 99DE-1049436.  
 XX  
 XX (SCHD ) SCHERING AG.  
 PA  
 XX Christophers E, Harder J, Schroeder J;  
 PI WPI; 2000-514948/46.  
 XX N-PSDB; AAA71753.  
 DR  
 DR New human antibiotic peptides, useful for treating microbial  
 PT infections, particularly when incorporated in wound dressings, also  
 PT related nucleic acid -  
 PT  
 XX Claim 1; Page 37; 41pp; German.  
 PS  
 XX This invention describes the novel active, mature human proteins (I)  
 CC SAP-2 and SAP-3 which have antibiotic, antibacterial, antifungal and  
 CC antiviral activity. (I), and their precursors, are useful for treating  
 CC or preventing microbial infections (caused by bacteria, fungi or  
 CC viruses), particularly where they (or human cells expressing them) are  
 CC included in wound dressings, and to produce specific antibodies (Ab) or  
 CC their fragments. Ab are used as diagnostic reagents, e.g. to detect a  
 CC deficiency of (I) or the presence of a (I) variant. This sequence  
 CC represents the mature human SAP-3 protein described in the method of the  
 CC invention.  
 XX  
 XX Sequence 45 AA;  
 SQ  
 Query Match 68.1%; Score 250; DB 21; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-23;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 GIINTLQKYCYVRGRCVAVLSCLPKPEQIGKCGTRGRKCCRRKK 67  
 DB 1 GIINTLQKYCYVRGRCVAVLSCLPKPEQIGKCGTRGRKCCRRKK 45  
 RESULT 9  
 AAO17767  
 ID AAO17767 standard; peptide; 45 AA.  
 XX  
 AC AAO17767;  
 XX  
 DT 30-AUG-2002 (first entry)  
 XX  
 DE Human beta-defensin-3 derivative #2.  
 XX  
 KW Human; beta-defensin-3; HBD-3; bacterial infection; gene therapy;  
 KW respiratory system; cystic fibrosis; inflammation; urogenital tract;  
 KW antibacterial; fungicide; cytostatic; antiinflammatory; antiulcer;  
 KW gastrointestinal tract; septicemia; apoptosis induction; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200240512-A2.  
 PN  
 XX 23-MAY-2002.  
 PD

XX 14-NOV-2001; 2001WO-EP13174.  
 PF  
 XX 14-NOV-2000; 2000DE-1056365.  
 PR  
 PR 30-MAR-2001; 2001DE-1016220.  
 XX  
 PA (IPFP-) IPF PHARM GMBH.  
 XX  
 XX Forssmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;  
 PI Maegert H;  
 XX WPI; 2002-435959/46.  
 DR  
 XX New human beta-defensin 3, useful for treating or preventing microbial  
 PT infection and tumors, also related nucleic acid -  
 PT  
 XX Claim 2; Page 23; 36pp; German.  
 PS  
 XX The present invention relates to human beta-defensin-3 (HBD-3) and its  
 CC derivatives. The peptide, its coding sequence and vectors containing the  
 CC coding sequence are useful in (gene) therapy and diagnosis, especially  
 CC for preventing or treating a wide range of microbial infections  
 CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the  
 CC respiratory tract, especially in cases of cystic fibrosis, and  
 CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal  
 CC and urogenital tracts, sepsis and yeast infections), and for inducing  
 CC apoptosis for treating malignant melanoma and tumours. The present  
 CC sequence is a derivative of human BD-3.  
 XX  
 XX Sequence 45 AA;  
 SQ  
 Query Match 68.1%; Score 250; DB 23; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-23;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 23 GIINTLQKYCYVRGRCVAVLSCLPKPEQIGKCGTRGRKCCRRKK 67  
 DB 1 GIINTLQKYCYVRGRCVAVLSCLPKPEQIGKCGTRGRKCCRRKK 45  
 RESULT 10  
 AAU09709  
 ID AAU09709 standard; Protein; 45 AA.  
 XX  
 AC AAU09709;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human beta-defensin-3 (HBD-3) mature protein sequence #2.  
 XX  
 XX Human; antimicrobial peptide; human beta-defensin-3; HBD-3;  
 KW microbial growth; microbial infection; pulmonary infection.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200192309-A2.  
 PN  
 XX 06-DEC-2001.  
 PD  
 XX 01-JUN-2001; 2001WO-US18057.  
 PF  
 PR 01-JUN-2000; 2000US-208792P.  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA  
 XX McCray PB, Tack B, Jia HP, Schutte BC;  
 PI WPI; 2002-106302/14.  
 DR  
 XX New human beta-defensin 3 peptides and nucleic acids encoding peptides,  
 PT useful for treating or preventing microbial growth or infection, or in  
 PT gene therapy -  
 PT  
 XX

PS Claim 29; Page 98; 110pp; English.

CC The present invention relates to the isolation of a novel antimicrobial  
CC peptide, human beta-defensin-3 (HBD-3). Also described is a method of  
CC inhibiting growth of a microbe by introducing into a host or environment  
CC the antimicrobial peptide of the invention. The peptide is useful for  
CC treating or preventing microbial growth or infections, e.g. pulmonary  
CC infections when administered by inhalation. The peptide can be applied  
CC on a work surface or a surgical instrument for the prevention and/or  
CC suppression of microbial growth. The present sequence represents  
CC HBD-3 mature protein sequence #2.

XX Sequence 45 AA;

Query Match 68.1%; Score 250; DB 23; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.3e-23;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYYCRVGRGCAVLSCLPKEQIGKSTRGKCCRRKK 67  
DB 1 GIINTLQKYYCRVGRGCAVLSCLPKEQIGKSTRGKCCRRKK 45

RESULT 11

AAU09708  
ID AAU09708 standard; Protein; 41 AA.

XX AC AAU09708;

XX DT 26-MAR-2002 (first entry)

XX DE Human beta-defensin-3 (HBD-3) mature protein sequence #1.

XX KW Human; antimicrobial peptide; human beta-defensin-3; HBD-3;  
XX microbial growth; microbial infection; pulmonary infection.

XX OS Homo sapiens.

XX PN WO200192309-A2.

XX PD 06-DEC-2001.

XX PF 01-JUN-2001; 2001WO-US18057.

XX PR 01-JUN-2000; 2000US-208792P.

XX PA (IOWA) UNIV IOWA RES FOUND.

XX PI McCray PB, Tack B, Jia HP, Schutte BC;

XX DR WPI; 2002-106302/14.

XX PT New human beta-defensin 3 peptides and nucleic acids encoding peptides,  
XX useful for treating or preventing microbial growth or infection, or in  
XX gene therapy.

XX PS Claim 28; Page 97; 110pp; English.

XX The present invention relates to the isolation of a novel antimicrobial  
XX peptide, human beta-defensin-3 (HBD-3). Also described is a method of  
XX inhibiting growth of a microbe by introducing into a host or environment  
XX the antimicrobial peptide of the invention. The peptide is useful for  
XX treating or preventing microbial growth or infections, e.g. pulmonary  
XX infections when administered by inhalation. The peptide can be applied  
XX on a work surface or a surgical instrument for the prevention and/or  
XX suppression of microbial growth. The present sequence represents  
XX HBD-3 mature protein sequence #1.

XX Sequence 41 AA;

Query Match 62.7%; Score 230; DB 23; Length 41;  
Best Local Similarity 100.0%; Pred. No. 6.1e-21;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TLQYYCRVGRGCAVLSCLPKEQIGKSTRGKCCRRKK 67  
DB 1 TLQYYCRVGRGCAVLSCLPKEQIGKSTRGKCCRRKK 41

RESULT 12

AAO17766

ID AAO17766 standard; peptide; 40 AA.

XX AC AAO17766;

XX DT 30-AUG-2002 (first entry)

XX DE Human beta-defensin-3 derivative #1.

XX KW Human; beta-defensin-3; HBD-3; bacterial infection; gene therapy;  
XX respiratory system; cystic fibrosis; inflammation; urogenital tract;  
XX antibacterial; fungicide; cytostatic; antiinflammatory; anticancer;  
XX gastrointestinal tract; septicemia; apoptosis induction; cancer.

XX OS Homo sapiens.

XX PN WO200240512-A2.

XX PD 23-MAY-2002.

XX PF 14-NOV-2001; 2001WO-EP13174.

XX PR 14-NOV-2000; 2000DE-1056365.

XX PR 30-MAR-2001; 2001DE-1016220.

XX PA (IPFP-) IPF PHARM GMBH.

XX PI Forssmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;  
XX Maegert H;

XX DR WPI; 2002-435959/46.

XX PT New human beta-defensin 3, useful for treating or preventing microbial  
XX infection and tumors, also related nucleic acid

XX PS Claim 2; Page 23; 36pp; German.

XX CC The present invention relates to human beta-defensin-3 (HBD-3) and its  
XX derivatives. The peptide, its coding sequence and vectors containing the  
XX coding sequence are useful in (gene) therapy and diagnosis, especially  
XX for preventing or treating a wide range of microbial infections  
XX (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the  
XX respiratory tract, especially in cases of cystic fibrosis, and  
XX Helicobacter pylori, also inflammatory diseases of the gastrointestinal  
XX tract and urogenital tracts, sepsis and yeast infections), and for inducing  
XX apoptosis for treating malignant melanoma and tumours. The present  
XX sequence is a derivative of human BD-3.

XX SQ Sequence 40 AA;

Query Match 61.3%; Score 225; DB 23; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.4e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LQYYCRVGRGCAVLSCLPKEQIGKSTRGKCCRRKK 67  
DB 1 LQYYCRVGRGCAVLSCLPKEQIGKSTRGKCCRRKK 40

RESULT 13

AAO17765

ID AAO17765 standard; peptide; 31 AA.

XX AC AAO17765;

XX DT 30-AUG-2002 (first entry)

XX DE Human beta-defensin-3.  
 XX KW Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;  
 KW respiratory system; cystic fibrosis; inflammation; urogenital tract;  
 KW antibacterial; fungicide; cytostatic; antiinflammatory; anticancer;  
 KW gastrointestinal tract; septicemia; apoptosis induction; cancer.  
 XX OS Homo sapiens.  
 XX PH Key Location/Qualifiers  
 FT Modified-site 1 /note= "may be linked to between 1 and 50 amino acids"  
 FT Modified-site 31  
 FT Modified-site /note= "may be linked to between 1 and 50 amino acids"  
 XX WO200240512-A2.  
 XX PD 23-MAY-2002.  
 XX PF 14-NOV-2001; 2001WO-EPI13174.  
 XX PR 14-NOV-2000; 2000DE-1056365.  
 XX PR 30-MAR-2001; 2001DE-1016220.  
 XX PA (IPPP-) IPP PHARM GMBH.  
 XX PI Forssmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;  
 PI Maegert H;  
 DR WPI; 2002-435959/46.  
 XX PT New human beta-defensin 3, useful for treating or preventing microbial  
 PT infection and tumors, also related nucleic acid -  
 XX Claim 1; Page 23; 36pp; German.  
 XX CC The present invention relates to human beta-defensin-3 (hBD-3) and its  
 CC derivatives. The peptide, its coding sequence and vectors containing the  
 CC coding sequence are useful in (gene) therapy and diagnosis, especially  
 CC for preventing or treating a wide range of microbial infections  
 CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the  
 CC respiratory tract, especially in cases of cystic fibrosis, and  
 CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal  
 CC and urogenital tracts, sepsis and yeast infections), and for inducing  
 CC apoptosis for treating malignant melanoma and tumours. The present  
 CC sequence is human BD-3.  
 XX SQ Sequence 31 AA;  
 Query Match 48.2%; Score 177; DB 23; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 33 CRVGGRCVAVLSCLPKPEQIGKSTRGRKCC 63  
 DB 1 CRVGGRCVAVLSCLPKPEQIGKSTRGRKCC 31  
 RESULT 14  
 AAM49572  
 ID AAM49572 standard; peptide; 31 AA.  
 XX AC AAM49572;  
 XX DT 28-MAY-2002 (first entry)  
 XX DE Human beta-defensin hBD-5 peptide fragment #1.  
 KW Defensin; human; antibacterial; antiinfertility; contraceptive;  
 KW peptide therapy; infection; gastrointestinal; respiratory tract;  
 KW urogenital tract; skin; gland; sperm penetration; systemic disease;  
 KW infertility; sperm inactivation; sperm maturation; diagnostic marker;

KW inflammatory disease; epithelial organ; gene therapy.  
 XX OS Homo sapiens.  
 XX PN WO200204487-A2.  
 XX PD 17-JAN-2002.  
 XX PF 11-JUL-2001; 2001WO-EP07973.  
 XX PR 11-JUL-2000; 2000DE-1033505.  
 XX PA (IPPP-) IPP PHARM GMBH.  
 XX PI Forssmann W, Conejo-Garcia J, Adermann K;  
 XX WPI; 2002-179697/23.  
 XX PT New defensin type peptides useful for treatment of bacterial infections  
 PT and for fertility control, and as a diagnostic marker of inflammatory  
 PT disease in epithelial organs -  
 XX Claim 2; Page 21; 41pp; German.  
 XX CC This invention describes novel peptides (I) of the defensin type which  
 CC have antibacterial, antiinfertility and contraceptive activity and which  
 CC can be used for peptide therapy. (II), and their derivatives and  
 CC fragments, are used: (i) to treat bacterial infections, particularly of  
 CC the gastrointestinal, respiratory or urogenital tracts, or of the skin  
 CC and associated glands; (ii) to treat systemic diseases associated with  
 CC overexpression or deficiency of defensin production, particularly as  
 CC substitution therapy or by using (i)-specific antibodies; (iii) to treat  
 CC infertility, especially where the result of disordered sperm penetration,  
 CC inactivation or maturation, also as contraceptives; and (iv) as a diagnostic  
 CC marker of inflammatory disease in epithelial organs. Both chronic and  
 CC acute diseases may be treated, e.g. in intensive care. Also genes that  
 CC encode (I) can be used for systemic or localised gene therapy of the  
 CC specified diseases, in epithelial tissues or organs. (I) have exceptional  
 CC biological activity and since they do not induce an immune response, they  
 CC are particularly well suited for long-term use. This sequence represents  
 CC a human defensin described in the disclosure of the invention.  
 XX SQ Sequence 31 AA;  
 Query Match 48.2%; Score 177; DB 23; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 33 CRVGGRCVAVLSCLPKPEQIGKSTRGRKCC 63  
 DB 1 CRVGGRCVAVLSCLPKPEQIGKSTRGRKCC 31  
 RESULT 15  
 AAM49576  
 ID AAM49576 standard; peptide; 31 AA.  
 XX AC AAM49576;  
 XX DT 28-MAY-2002 (first entry)  
 XX DE Human beta-defensin hBD-6 peptide fragment #2.  
 KW Defensin; human; antibacterial; antiinfertility; contraceptive;  
 KW peptide therapy; infection; gastrointestinal; respiratory tract;  
 KW urogenital tract; skin; gland; sperm penetration; systemic disease;  
 KW infertility; sperm inactivation; sperm maturation; diagnostic marker;  
 KW inflammatory disease; epithelial organ; gene therapy.  
 XX OS Homo sapiens.  
 XX PN WO200204487-A2.  
 XX

PD 17-JAN-2002.  
 XX  
 PF 11-JUL-2001; 2001WO-BP07973.  
 XX  
 PR 11-JUL-2000; 2000DE-1033505.  
 XX  
 PA (IPFP-) IPF PHARM GMBH.  
 XX  
 PI Forssmann W, Conejo-Garcia J, Adermann K;  
 XX  
 DR WPI; 2002-179697/23.  
 XX  
 XX New defensin type peptides useful for treatment of bacterial infections  
 PT and for fertility control, and as a diagnostic marker of inflammatory  
 PT disease in epithelial organs -  
 XX  
 XX  
 PS Claim 3; Page 22; 41pp; German.  
 XX  
 XX This invention describes novel peptides (I) of the defensin type which  
 CC have antibacterial, antifertility and contraceptive activity and which  
 CC can be used for peptide therapy. (i), and their derivatives and  
 CC fragments, are used: (i) to treat bacterial infections, particularly of  
 CC the gastrointestinal, respiratory or urogenital tracts, or of the skin  
 CC and associated glands; (ii) to treat systemic diseases associated with  
 CC overexpression or deficiency of defensin production, particularly as  
 CC substitution therapy or by using (I)-specific antibodies; (iii) to treat  
 CC infertility, especially where the result of disordered sperm penetration,  
 CC initiation or maturation, also as contraceptives; and (iv) as a diagnostic  
 CC marker of inflammatory disease in epithelial organs. Both chronic and  
 CC acute diseases may be treated, e.g. in intensive care. Also genes that  
 CC encode (I) can be used for systemic or localised gene therapy of the  
 CC specified diseases, in epithelial tissues or organs. (I) have exceptional  
 CC biological activity and since they do not induce an immune response, they  
 CC are particularly well suited for long-term use. This sequence represents  
 CC a human defensin described in the disclosure of the invention.  
 XX  
 SQ Sequence 31 AA;  
 Query Match 48.2%; Score 177; DB 23; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 33 CRVRGGRCVLSCLPKKEQIGKCKSTRGRKCC 63  
 DB 1 CRVRGGRCVLSCLPKKEQIGKCKSTRGRKCC 31  
 Search completed: October 31, 2003, 14:01:30  
 Job time : 84 secs



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: October 31, 2003, 14:01:37 ; Search time 29 Seconds  
(without alignments)  
97.753 Million cell updates/sec

Title: US-09-872-852-2

Perfect score: 367

Sequence: 1 MRIHYLLPALLFLVVPFG.....KEEQIGKSTRGKCRKK 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/ptodata/2/iaa/PTUS COMB.pcp.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	367	100.0	67	4	US-09-868-659-4
2	367	100.0	67	4	US-09-868-659-4
3	357	97.3	65	4	US-09-868-659-2
4	250	68.1	45	4	US-09-868-659-2
5	241	65.7	49	4	US-09-868-659-2
6	236	64.3	48	4	US-09-868-659-2
7	234	63.8	48	4	US-09-868-659-2
8	229	62.4	47	4	US-09-868-659-2
9	228	62.1	47	4	US-09-868-659-2
10	223	60.8	46	4	US-09-868-659-2
11	220	59.9	46	4	US-09-868-659-2
12	215	58.6	45	4	US-09-868-659-2
13	214	58.3	45	4	US-09-868-659-2
14	209	56.9	44	4	US-09-868-659-2
15	208	56.7	44	4	US-09-868-659-2
16	208	56.7	44	4	US-09-868-659-2
17	204	55.6	43	4	US-09-868-659-2
18	204	55.6	43	4	US-09-868-659-2
19	203	55.3	43	4	US-09-868-659-2
20	203	55.3	43	4	US-09-868-659-2
21	200	54.5	42	4	US-09-868-659-2
22	200	54.5	42	4	US-09-868-659-2
23	199	54.2	42	4	US-09-868-659-2
24	199	54.2	42	4	US-09-868-659-2
25	198	54.0	42	4	US-09-868-659-2
26	195	53.1	41	4	US-09-868-659-2
27	195	53.1	41	4	US-09-868-659-2

28	194	52.9	41	4	US-09-636-399A-25
29	194	52.9	41	4	US-09-636-399A-29
30	194	52.9	41	4	US-09-636-399A-51
31	190	51.8	40	4	US-09-636-399A-28
32	189	51.5	40	4	US-09-636-399A-30
33	189	51.5	40	4	US-09-636-399A-32
34	189	51.5	40	4	US-09-636-399A-52
35	189	51.5	40	4	US-09-636-399A-53
36	185	50.4	39	4	US-09-636-399A-19
37	185	50.4	39	4	US-09-636-399A-55
38	184	50.1	39	4	US-09-636-399A-31
39	184	50.1	39	4	US-09-636-399A-33
40	184	50.1	39	4	US-09-636-399A-54
41	182	49.6	38	4	US-09-636-399A-59
42	182	49.6	38	4	US-09-636-399A-57
43	180	49.0	38	4	US-09-636-399A-18
44	180	49.0	38	4	US-09-636-399A-56
45	179	48.8	38	4	US-09-636-399A-34

## ALIGNMENTS

RESULT 1  
US-09-868-659-4  
; Sequence 4, Application US/09868659  
; Patent No. 6568002  
; GENERAL INFORMATION:  
; APPLICANT: CHRISTOPHERS, ENNO  
; APPLICANT: HARDER, JURGEN  
; APPLICANT: SCHRODER, JENS  
; TITLE OF INVENTION: HUMAN ANTIBIOTIC PROTEINS  
; FILE REFERENCE: SCH-1813A  
; CURRENT APPLICATION NUMBER: US/09/868,659  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: PCT/EP00/00776  
; PRIOR FILING DATE: 2000-02-01  
; PRIOR APPLICATION NUMBER: DE 199 05 128.9  
; PRIOR FILING DATE: 1999-02-01  
; PRIOR APPLICATION NUMBER: DE 199 49 436.3  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-868-659-4

Query Match 100.0%; Score 367; DB 4; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2e+38;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRIHYLLPALLFLVVPFGHGGIINTLQKYCRVGRGCAVLSCLPKEEQIGKSTRGR 60  
DB 1 MRIHYLLPALLFLVVPFGHGGIINTLQKYCRVGRGCAVLSCLPKEEQIGKSTRGR 60  
QY 61 KCCRKK 67  
DB 61 KCCRKK 67

RESULT 2  
US-09-636-399A-10  
; Sequence 10, Application US/09636399A  
; Patent No. 6576755  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baidur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS

```
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-399A-10

Query Match      100.0%; Score 367; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTRGR 60
DB 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTRGR 60
QY 61 KCCRRK 67
DB 61 KCCRRK 67

RESULT 3
US-09-636-399A-2
Sequence 2, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 65
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-399A-2

Query Match      97.3%; Score 357; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.3e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTRGR 60
DB 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTRGR 60
QY 61 KCCRR 65
DB 61 KCCRR 65

us-09-868-659-2
Sequence 2, Application US/09868659
Patent No. 6568002
GENERAL INFORMATION:
APPLICANT: CHRISTOPHERS, ENNO
APPLICANT: HARDER, JURGEN
APPLICANT: SCHROEDER, JENS
TITLE OF INVENTION: HUMAN ANTIBIOTIC PROTEINS
FILE REFERENCE: SCH-1813A
CURRENT APPLICATION NUMBER: US/09/868,659
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: PCT/EP00/00776
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: DE 199 05 128.9
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: DE 199 49 436.3
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 45
TYPE: PRT
ORGANISM: Homo sapiens
US-09-868-659-2

Query Match      68.1%; Score 250; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 3.9e-24;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTRGRKCCRRK 67
DB 1 GIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTRGRKCCRRK 45

RESULT 5
US-09-636-399A-35
Sequence 35, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 49
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (45)...(45)
OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-35

Query Match      65.7%; Score 241; DB 4; Length 49;
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Best Local Similarity 91.8%; Pred. No. 5.6e-23;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 PGHGGIINTLQKYCYVRGRCVAVLSCLPKPEEQIGKSTGRKCCRRK 67
Db 1 PGHGGIINTLQYCYVRGRCVAVLSCLPKPEECIGKMTGRKCCRRK 49

RESULT 6
US-09-636-399A-36
; Sequence 36, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636.399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (45)...(45)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-36

Query Match 64.3%; Score 236; DB 4; Length 48;
Best Local Similarity 91.7%; Pred. No. 2.3e-22;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 PGHGGIINTLQKYCYVRGRCVAVLSCLPKPEEQIGKSTGRKCCRRK 66
Db 1 PGHGGIINTLQYCYVRGRCVAVLSCLPKPEECIGKMTGRKCCRRK 48

RESULT 7
US-09-636-399A-37
; Sequence 37, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636.399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (44)...(44)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met.
US-09-636-399A-37

Query Match 62.4%; Score 229; DB 4; Length 47;
Best Local Similarity 91.5%; Pred. No. 1.6e-21;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 GHGGIINTLQKYCYVRGRCVAVLSCLPKPEEQIGKSTGRKCCRRK 66
Db 1 GHGGIINTLQYCYVRGRCVAVLSCLPKPEECIGKMTGRKCCRRK 47

RESULT 8
US-09-636-399A-38
; Sequence 38, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636.399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (44)...(44)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met.
US-09-636-399A-38

Query Match 63.8%; Score 234; DB 4; Length 48;
Best Local Similarity 91.7%; Pred. No. 4e-22;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 GHGGIINTLQKYCYVRGRCVAVLSCLPKPEEQIGKSTGRKCCRRK 67
Db 1 GHGGIINTLQYCYVRGRCVAVLSCLPKPEECIGKMTGRKCCRRK 48

RESULT 9
US-09-636-399A-39
; Sequence 39, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
```

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; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (43)...(43)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-39

Query Match      62.1%; Score 228; DB 4; Length 47;
Best Local Similarity 91.5%; Pred. No. 2.2e-21;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 21 HGGIINTLQKYCRVGRGCAVLSCLPKPEQIGKSTGRKCCRRKK 67
Db 1 HGGIINTLQYCYCRVGRGCAVLSCLPKPEECIGRMSTGRKCCRRKK 47
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RESULT 10
US-09-636-399A-40
; Sequence 40, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (43)...(43)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-40
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Query Match      60.8%; Score 223; DB 4; Length 46;
Best Local Similarity 91.3%; Pred. No. 8.9e-21;
Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 21 HGGIINTLQKYCYCRVGRGCAVLSCLPKPEQIGKSTGRKCCRRKK 66
Db 1 HGGIINTLQYCYCRVGRGCAVLSCLPKPEECIGRMSTGRKCCRRKK 46

RESULT 11
US-09-636-399A-41
; Sequence 41, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (42)...(42)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-41
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Query Match      59.9%; Score 220; DB 4; Length 46;
Best Local Similarity 91.3%; Pred. No. 2.1e-20;
Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 22 GGIINTLQKYCYCRVGRGCAVLSCLPKPEQIGKSTGRKCCRRKK 67
Db 1 GGIINTLQYCYCRVGRGCAVLSCLPKPEECIGRMSTGRKCCRRKK 46

RESULT 12
US-09-636-399A-42
; Sequence 42, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Defensin polypeptide  
; NAME/KEY: VARIANT  
; LOCATION: (42)...(42)  
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met  
US-09-636-399A-42

Query Match 58.6%; Score 215; DB 4; Length 45;  
Best Local Similarity 91.1%; Pred. No. 8.5e-20;  
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 22 GGINTLQKYCRVGRGCAVLSCLPKKEQIGKSTRGKCCRRK 66  
DB 1 GGINTLQLYYCRVGRGCAVLSCLPKKECIGKSTRGKCCRRK 45

RESULT 13  
US-09-636-399A-43

; Sequence 43, Application US/09636399A  
; Patent No. 6576755  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baindur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44C2  
; CURRENT APPLICATION NUMBER: US/09/636,399A  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/058,335  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Defensin polypeptide  
; NAME/KEY: VARIANT  
; LOCATION: (41)...(41)  
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met  
US-09-636-399A-43

Query Match 58.3%; Score 214; DB 4; Length 45;  
Best Local Similarity 91.1%; Pred. No. 1.1e-19;  
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 23 GIINTLQKYCRVGRGCAVLSCLPKKEQIGKSTRGKCCRRK 67  
DB 1 GIINTLQLYYCRVGRGCAVLSCLPKKECIGKSTRGKCCRRK 45

RESULT 14  
US-09-636-399A-44

; Sequence 44, Application US/09636399A  
; Patent No. 6576755  
; GENERAL INFORMATION:

; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baindur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44C2  
; CURRENT APPLICATION NUMBER: US/09/636,399A  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/058,335  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 44  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Defensin polypeptide  
; NAME/KEY: VARIANT  
; LOCATION: (41)...(41)  
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met  
US-09-636-399A-44

Query Match 56.9%; Score 209; DB 4; Length 44;  
Best Local Similarity 90.9%; Pred. No. 4.6e-19;  
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 23 GIINTLQKYCRVGRGCAVLSCLPKKEQIGKSTRGKCCRRK 66  
DB 1 GIINTLQLYYCRVGRGCAVLSCLPKKECIGKSTRGKCCRRK 44

RESULT 15

US-09-636-399A-20  
; Sequence 20, Application US/09636399A  
; Patent No. 6576755  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baindur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44C2  
; CURRENT APPLICATION NUMBER: US/09/636,399A  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/058,335  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Defensin Polypeptide  
US-09-636-399A-20

Query Match 56.7%; Score 208; DB 4; Length 44;  
Best Local Similarity 90.9%; Pred. No. 6.1e-19;

	Matches	40;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
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Db	1	IINTLQKYYCRVGRCAVLSCLPKEQIGKCTRGRKCCRRKK 44								

Search completed: October 31, 2003, 14:05:39  
Job time : 29 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 31, 2003, 14:00:07 ; Search time 28 Seconds  
(without alignments)  
409.528 Million cell updates/sec

Title: US-09-872-852-2  
Perfect score: 367  
Sequence: 1 MRIHYLLFALLFLVPPG.....KEEQIGKSTRGKCCRRK 67

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 642050 seqs, 171146064 residues

Total number of hits satisfying chosen parameters: 642050

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	367	100.0	67	9	US-09-917-340-52
2	367	100.0	67	9	US-09-917-340-72
3	367	100.0	67	10	US-09-872-852-2
4	367	100.0	67	12	US-10-091-166B-10
5	367	100.0	67	12	US-10-272-121-10
6	367	100.0	67	12	US-10-409-366-10
7	367	100.0	67	12	US-10-409-532-10
8	357	97.3	65	12	US-10-091-166B-2
9	357	97.3	65	12	US-10-272-121-2
10	357	97.3	65	12	US-10-409-366-2
11	357	97.3	65	12	US-10-409-532-2
12	250	68.1	45	10	US-09-872-852-4
13	241	65.7	49	12	US-10-091-166B-35
14	241	65.7	49	12	US-10-272-121-35
15	241	65.7	49	12	US-10-409-366-35

16	241	65.7	49	12	US-10-409-532-35	Sequence 35, Appl
17	236	64.3	48	12	US-10-091-166B-36	Sequence 36, Appl
18	236	64.3	48	12	US-10-272-121-36	Sequence 36, Appl
19	236	64.3	48	12	US-10-409-366-36	Sequence 36, Appl
20	236	64.3	48	12	US-10-409-532-36	Sequence 36, Appl
21	234	63.8	48	12	US-10-091-166B-37	Sequence 37, Appl
22	234	63.8	48	12	US-10-272-121-37	Sequence 37, Appl
23	234	63.8	48	12	US-10-409-366-37	Sequence 37, Appl
24	234	63.8	48	12	US-10-409-532-37	Sequence 37, Appl
25	230	62.7	41	10	US-09-872-852-3	Sequence 3, Appl
26	229	62.4	47	12	US-10-091-166B-38	Sequence 38, Appl
27	229	62.4	47	12	US-10-272-121-38	Sequence 38, Appl
28	229	62.4	47	12	US-10-409-366-38	Sequence 38, Appl
29	229	62.4	47	12	US-10-409-532-38	Sequence 38, Appl
30	228	62.1	47	12	US-10-091-166B-39	Sequence 39, Appl
31	228	62.1	47	12	US-10-272-121-39	Sequence 39, Appl
32	228	62.1	47	12	US-10-409-366-39	Sequence 39, Appl
33	228	62.1	47	12	US-10-409-532-39	Sequence 39, Appl
34	223	60.8	46	12	US-10-091-166B-40	Sequence 40, Appl
35	223	60.8	46	12	US-10-272-121-40	Sequence 40, Appl
36	223	60.8	46	12	US-10-409-366-40	Sequence 40, Appl
37	223	60.8	46	12	US-10-409-532-40	Sequence 40, Appl
38	220	59.9	46	12	US-10-091-166B-41	Sequence 41, Appl
39	220	59.9	46	12	US-10-272-121-41	Sequence 41, Appl
40	220	59.9	46	12	US-10-409-366-41	Sequence 41, Appl
41	220	59.9	46	12	US-10-409-532-41	Sequence 41, Appl
42	215	58.6	45	12	US-10-091-166B-42	Sequence 42, Appl
43	215	58.6	45	12	US-10-272-121-42	Sequence 42, Appl
44	215	58.6	45	12	US-10-409-366-42	Sequence 42, Appl
45	215	58.6	45	12	US-10-409-532-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1  
US-09-917-340-52  
; Sequence 52, Application US/09917340  
; Patent No. US20020090369A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Christopher J.  
; APPLICANT: McAnulty, Jonathan F.  
; APPLICANT: Reid, Ted W.  
; TITLE OF INVENTION: Transplant Media  
; FILE REFERENCE: TPLANT-06468  
; CURRENT APPLICATION NUMBER: US/09/917,340  
; PRIOR FILING DATE: 2001-07-29  
; PRIOR APPLICATION NUMBER: 60/221,632  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: 60/249,602  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/290,932  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 52  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-917-340-52

Query Match 100.0%; Score 367; DB 9; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRIHYLLFALLFLVPPVPGGGIINTLQKYCYVRGRCVAVLSCLPKEEQIGKSTRGR 60  
DB 1 MRIHYLLFALLFLVPPVPGGGIINTLQKYCYVRGRCVAVLSCLPKEEQIGKSTRGR 60  
QY 61 KCCRRKK 67  
DB 61 KCCRRKK 67

RESULT 2  
US-09-917-340-72  
; Sequence 72, Application US/09917340  
; Patent No. US20020090369A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Christopher J.  
; APPLICANT: McAnulty, Jonathan F.  
; APPLICANT: Reid, Ted W.  
; TITLE OF INVENTION: Transplant Media  
; FILE REFERENCE: TELANT-06468  
; CURRENT APPLICATION NUMBER: US/09/917,340  
; CURRENT FILING DATE: 2001-07-29  
; PRIOR APPLICATION NUMBER: 60/221,632  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: 60/249,602  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/290,932  
; PRIOR FILING DATE: 2001-03-15  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 72  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-917-340-72

Query Match 100.0%; Score 367; DB 9; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYCYRVRGRCVAVLSCLPKEQIGKCTRGR 60  
Db 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYCYRVRGRCVAVLSCLPKEQIGKCTRGR 60  
Qy 61 KCCRRKK 67  
Db 61 KCCRRKK 67

RESULT 3  
US-09-872-852-2  
; Sequence 2, Application US/09872852  
; Patent No. US20020115602A1  
; GENERAL INFORMATION:  
; APPLICANT: MCCRAY JR, PAUL B.  
; APPLICANT: TACK, BRIAN  
; APPLICANT: JIA, HONG PENG  
; APPLICANT: SCHUTTE, BRIAN C.  
; TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC  
; FILE REFERENCE: IOWA:031US  
; CURRENT APPLICATION NUMBER: US/09/872,852  
; CURRENT FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: 60/208,792  
; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-872-852-2

Query Match 100.0%; Score 367; DB 10; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYCYRVRGRCVAVLSCLPKEQIGKCTRGR 60  
Db 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYCYRVRGRCVAVLSCLPKEQIGKCTRGR 60

Db 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYCYRVRGRCVAVLSCLPKEQIGKCTRGR 60  
Qy 61 KCCRRKK 67  
Db 61 KCCRRKK 67  
RESULT 4  
US-10-091-166B-10  
; Sequence 10, Application US/10091166B  
; Publication No. US20030143671A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baindur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44D1  
; CURRENT APPLICATION NUMBER: US/10/091,166B  
; CURRENT FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: US 09/344,097  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: US 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: US 60/058,335  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-091-166B-10

Query Match 100.0%; Score 367; DB 12; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYCYRVRGRCVAVLSCLPKEQIGKCTRGR 60  
Db 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYCYRVRGRCVAVLSCLPKEQIGKCTRGR 60  
Qy 61 KCCRRKK 67  
Db 61 KCCRRKK 67

RESULT 5  
US-10-272-121-10  
; Sequence 10, Application US/10272121  
; Publication No. US20030157638A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baindur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44D2  
; CURRENT APPLICATION NUMBER: US/10/272,121  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: US 09/344,097  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: US 60/064,294



```

; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-121-10

```

```

Query Match      100.0%; Score 367; DB 12; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVVPVGHGGIINTLQKYCRVGRGCAVLSCLPKKEQIGKSTRGR 60
   |||||||
Db 1 MRIHYLLFALLFLVVPVGHGGIINTLQKYCRVGRGCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRKK 67
   |||||||
Db 61 KCCRKK 67

```

```

RESULT 6
US-10-409-366-10
; Sequence 10, Application US/10409366
; Publication No. US20030166912A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/10/409,366
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-409-366-10

```

```

Query Match      100.0%; Score 367; DB 12; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVVPVGHGGIINTLQKYCRVGRGCAVLSCLPKKEQIGKSTRGR 60
   |||||||
Db 1 MRIHYLLFALLFLVVPVGHGGIINTLQKYCRVGRGCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRKK 67
   |||||||
Db 61 KCCRKK 67

```

```

RESULT 7
US-10-409-532-10
; Sequence 10, Application US/10409532
; Publication No. US20030166913A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/10/409,532
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-409-532-10

```

```

Query Match      100.0%; Score 367; DB 12; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVVPVGHGGIINTLQKYCRVGRGCAVLSCLPKKEQIGKSTRGR 60
   |||||||
Db 1 MRIHYLLFALLFLVVPVGHGGIINTLQKYCRVGRGCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRKK 67
   |||||||
Db 61 KCCRKK 67

```

```

RESULT 8
US-10-091-166B-2
; Sequence 2, Application US/10091166B
; Publication No. US20030143671A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44D1
; CURRENT APPLICATION NUMBER: US/10/091,166B
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/636,399
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/344,097
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-166B-2

```

```
Query Match          97.3%; Score 357; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.1e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCSTRGR 60
Db 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCSTRGR 60

Qy 61 KCCR 65
Db 61 KCCR 65

RESULT 9
US-10-272-121-2
; Sequence 2, Application US/10272121
; Publication No. US20030157638A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/10/272,121
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/636,399
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/344,097
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-121-2

Query Match          97.3%; Score 357; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.1e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCSTRGR 60
Db 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCSTRGR 60

Qy 61 KCCR 65
Db 61 KCCR 65

RESULT 10
US-10-409-366-2
; Sequence 2, Application US/10409366
; Publication No. US20030166912A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/10/409,366
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/636,399A
```

```
Query Match          97.3%; Score 357; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.1e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCSTRGR 60
Db 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCSTRGR 60

Qy 61 KCCR 65
Db 61 KCCR 65

RESULT 11
US-10-409-532-2
; Sequence 2, Application US/10409532
; Publication No. US20030166913A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/10/409,532
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-409-532-2

Query Match          97.3%; Score 357; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.1e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCSTRGR 60
Db 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCSTRGR 60

Qy 61 KCCR 65
Db 61 KCCR 65
```

```
RESULT 12
US-09-872-852-4
; Sequence 4, Application US/09872852
; Patent No. US20020115602A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY JR, PAUL B.
; APPLICANT: TACK, BRIAN
; APPLICANT: JIA, HONG PENG
; APPLICANT: SCHUTTE, BRIAN C.
; TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
; FILE REFERENCE: BETA-DEFENSIN ANTIMICROBIAL PEPTIDE
; CURRENT APPLICATION NUMBER: US/09/872,852
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,792
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 4
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-872-852-4

Query Match      68.1%; Score 250; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.4e-23; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 0;

QY 23 GIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 67
      |||||
Db 1 GIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 45

RESULT 13
US-10-091-166B-35
; Sequence 35, Application US/10091166B
; Publication No. US20030143671A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44D1
; CURRENT APPLICATION NUMBER: US/10/091,166B
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/636,399
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/344,097
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (45)...(45)
; OTHER INFORMATION: leucine, isoleucine, valine, phenylalanine, or
; OTHER INFORMATION: methionine
US-10-091-166B-35

Query Match      65.7%; Score 241; DB 12; Length 49;
Best Local Similarity 91.8%; Pred. No. 3.3e-22; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 4;

QY 19 PGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 67
      |||||
Db 1 PGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 49

RESULT 15
US-10-409-366-35
; Sequence 35, Application US/10409366
; Publication No. US20030166912A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
US-10-409-366-35

Query Match      65.7%; Score 241; DB 12; Length 49;
Best Local Similarity 91.8%; Pred. No. 3.3e-22; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 4;

QY 19 PGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 67
      |||||
Db 1 PGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 49
```

```
; OTHER INFORMATION: leucine, isoleucine, valine, phenylalanine, or
; OTHER INFORMATION: methionine
US-10-091-166B-35

Query Match      65.7%; Score 241; DB 12; Length 49;
Best Local Similarity 91.8%; Pred. No. 3.3e-22; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 4;

QY 19 PGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 67
      |||||
Db 1 PGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 49

RESULT 14
US-10-272-121-35
; Sequence 35, Application US/10272121
; Publication No. US20030157638A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44D2
; CURRENT APPLICATION NUMBER: US/10/272,121
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/636,399
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/344,097
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (45)...(45)
; OTHER INFORMATION: leucine, isoleucine, valine, phenylalanine, or
; OTHER INFORMATION: methionine
US-10-272-121-35

Query Match      65.7%; Score 241; DB 12; Length 49;
Best Local Similarity 91.8%; Pred. No. 3.3e-22; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 4;

QY 19 PGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 67
      |||||
Db 1 PGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 49

RESULT 15
US-10-409-366-35
; Sequence 35, Application US/10409366
; Publication No. US20030166912A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
US-10-409-366-35

Query Match      65.7%; Score 241; DB 12; Length 49;
Best Local Similarity 91.8%; Pred. No. 3.3e-22; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 4;

QY 19 PGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 67
      |||||
Db 1 PGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKSTGRKCCRRKK 49
```

```

; CURRENT APPLICATION NUMBER: US/10/409,366
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (45)...(45)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-10-409-366-35

```

```

Query Match      65.7%; Score 241; DB 12; Length 49;
Best Local Similarity 91.8%; Pred. No. 3.3e-22;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      19 PCHGGIINTLQKYCRVRGRCVAVLSCLPKKEQIGKSTGRKCKRRKK 67
      |||||
Db      1 PCHGGIINTLQLYYCRVRGRCVAVLSCLPKKECIGKMKSTGRKCKRRKK 49

```

```

Search completed: October 31, 2003, 14:05:03
Job time : 29 secs

```

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: October 31, 2003, 13:59:27 ; Search time 40 Seconds  
(without alignments)  
161.083 Million cell updates/sec

Title: US-09-872-852-2

Perfect score: 367

Sequence: 1 MRIHYLLFALLFLVLPVPG.....KBEQIGKSTRGKCCRKK 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

PTR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	30.8	64	2 A56128	lingual antimicrobial
2	111	30.2	64	2 A47438	airway epithelial
3	108	29.4	65	2 C35947	crocamine 3 precu
4	108	29.4	65	2 C35947	crocamine 1 precu
5	103	28.1	65	2 JCS324	myotoxin a precu
6	89	24.3	42	2 P45495	beta-defensin-6 -
7	83.5	22.8	64	2 B35947	crocamine 2 precu
8	75	20.4	38	2 B47753	beta-defensin-11 -
9	71	19.3	42	2 C45495	beta-defensin-3 -
10	69.5	18.9	45	2 A37909	myotoxin - eastern
11	69.5	18.9	95	1 WTRBM1	macrophage antibio
12	69	18.8	40	2 G45495	beta-defensin-7 -
13	69	18.8	40	2 I45495	beta-defensin-9 -
14	68	18.5	42	2 D47753	beta-defensin-13 -
15	66.5	18.1	43	1 CXRSCH	toxic peptide C -
16	65.5	17.8	42	1 CXRSMT	crocamine - tropic
17	65.5	17.8	51	2 D35947	crocamine 4 precu
18	65.5	17.8	95	1 WTRBM2	defensin CS-4 prec
19	62.5	17.0	42	1 MXRSMV	myotoxin a 6 - pra
20	61	16.6	122	2 JC6548	high sulfur protei
21	61	16.6	218	2 T22661	hypothetical prote
22	61	16.6	524	2 S38539	disintegrin-like m
23	61	16.6	670	2 I65967	disintegrin-like m
24	60.5	16.5	40	2 C39560	myotoxin a 5 - pra
25	60	16.3	32	2 E59076	defensin alpha-5 -
26	60	16.3	32	2 G59076	defensin alpha-7 -
27	60	16.3	33	2 D59076	defensin alpha-4 -
28	60	16.3	33	2 F59076	defensin alpha-6 -
29	60	16.3	855	2 T05981	hypothetical prote

30 59.5 16.2 260 2 AD2461 hypothetical prote  
31 59.5 16.2 454 2 B82412 probable magnesium  
32 59.5 16.2 1184 2 T09484 cartilage intermed  
33 59 16.1 40 2 E45495 beta-defensin-5 -  
34 59 16.1 177 2 S37650 high-sulfur kerati  
35 59 16.1 263 2 S57346 interleukin 15 rec  
36 58.5 15.9 43 2 A29089 myotoxin I - midge  
37 58.5 15.9 45 2 S12909 hypothetical prote  
38 58.5 15.9 88 2 H69475 colipase precursor  
39 58.5 15.9 112 2 A46717 F9K20.25 limporred  
40 58.5 15.9 359 2 A36816 probable finger pr  
41 58.5 15.9 705 2 S38066 corticostatic pept  
42 58 15.8 34 2 C49195 protamine - mouse  
43 58 15.8 51 1 HSMSS1 protamine 1 - rat  
44 58 15.8 51 2 S03997 high-sulfur wool m  
45 58 15.8 152 2 I47109

## ALIGNMENTS

### RESULT 1

A56128 lingual antimicrobial peptide precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Nov-1999

C:Accession: A56128; B56128

R:Schonwetter, B.S.; Stolzenberg, E.D.; Zasloff, M.A.

Science 267, 1645-1648, 1995

A:Title: Epithelial antibiotics induced at sites of inflammation.

A:Reference number: A56128; MUID:95192714; PMID:7886453

A:Accession: A56128

A:Molecule type: mRNA

A:Residues: 1-64 <SCH>

A:Cross-references: GB:S76279; NID:9894208; PIDN:AAB33727.1; PID:9894209

A:Accession: B56128

A:Molecule type: protein

A:Residues: 23-64 <SC2>

C:Keywords: antibacterial; antifungal

F:1-20/Domain: signal sequence #status predicted <SIG>

F:23-64/Product: lingual antimicrobial peptide #status experimental <MAT>

Query Match 30.8%; Score 113; DB 2; Length 64;

Best Local Similarity 42.4%; Pred. No. 5e-06;

Matches 28; Conservative 3; Mismatches 33; Indels 2; Gaps 1;

QY 1 MRIHYLLFALLFLVLPVPGHGGINTLQKYCYVRGRCVLSCLPKKEQIGKSTRGR 60

DB 1 MRLHLLALLFLVL--SAGSGFTQGVNSQSCRRNKIGICVPICPGSMRQIGTCLGAQV 58

QY 61 KCCRKK 66

DB 59 KCCRKK 64

### RESULT 2

A47438 airway epithelial antimicrobial peptide TAP precursor - bovine

N:Alternate names: antimicrobial peptide, tracheal

C:Species: Bos primigenius taurus (cattle)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999

C:Accession: A47438; A39397

R:Diamond, G.; Jones, D.E.; Bevins, C.L.

Proc. Natl. Acad. Sci. U.S.A. 90, 4596-4600, 1993

A:Title: Airway epithelial cells are the site of expression of a mammalian antimicrobial

A:Reference number: A47438; MUID:93281626; PMID:8506305

A:Accession: A47438

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-64 <DIA>

A:Cross-references: GB:L13373; NID:9289395; PIDN:AAA72363.1; PID:9289396

R:Diamond, G.; Zasloff, M.; Eck, H.; Brasseur, M.; Maloy, W.L.; Bevins, C.L.

Proc. Natl. Acad. Sci. U.S.A. 88, 3952-3956, 1991

A;Title: Tracheal antimicrobial peptide, a cysteine-rich peptide from mammalian tracheal

A;Reference number: A39397; MUID:91219490; PMID:2023943  
 A;Accession: A39397  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-64 <DI2>  
 A;Cross-references: GB:M63023; NID:g22226433; PIDN:AAB61757.1; PID:g163740  
 C;Genetics:  
 A;Introns: 19/2  
 P;1-26/Domain: signal sequence #status predicted <SIG>  
 P;27-64/Product: airway epithelial antimicrobial peptide TAP #status predicted <MAT>

Query Match 30.2%; Score 111; DB 2; Length 64;  
 Best Local Similarity 41.8%; Pred. No. 8.4e-06;  
 Matches 28; Conservative 7; Mismatches 28; Indels 4; Gaps 2;

Qy 1 MRHYLLFALLFLFVLPVPGH-GGIINTLQKYCRVGRGCAVLSCLPKEQIGK-STRG 59

Db 1 MRLHLLFALLFLFVLPVPGH-GGIINTLQKYCRVGRGCAVLSCLPKEQIGK-STRG 57

Qy 60 RKCCRRK 66

Db 58 VKCCRRK 64

#### RESULT 3

C35947  
 A;Title: crotoxin - tropical rattlesnake  
 C;Species: Crocalus durissus terrificus (tropical rattlesnake, cascabel)  
 C;Date: 14-Dec-1990 #sequence\_revision 14-Dec-1990 #text\_change 24-Jun-1993  
 C;Accession: C35947

R;Smith, L.A.; Schmidt, J.J.  
 Toxicol 28, 575-585, 1990

A;Title: Cloning and nucleotide sequences of crotoxin genes.

A;Reference number: A35947; MUID:90357261; PMID:2389256

A;Accession: C35947

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-65 <SMI>

C;Superfamily: crotoxin

Query Match 29.4%; Score 108; DB 2; Length 65;  
 Best Local Similarity 39.1%; Pred. No. 1.9e-05;  
 Matches 27; Conservative 9; Mismatches 21; Indels 12; Gaps 5;

Qy 1 MRHYLLFALLFLFVLPVPGH-GGIINTLQKYCRVGRGCAVLSCLPKEQIGK-STRG 56

Db 1 MKLYLLFALLFLFVLPVPGH-GGIINTLQKYCRVGRGCAVLSCLPKEQIGK-STRG 53

Qy 57 TRGRKCCRR 65

Db 54 WR-RKCCCK 61

#### RESULT 4

A35947  
 A;Title: crotoxin - tropical rattlesnake  
 C;Species: Crocalus durissus terrificus (tropical rattlesnake, cascabel)  
 C;Date: 14-Dec-1990 #sequence\_revision 14-Dec-1990 #text\_change 24-Jun-1993  
 C;Accession: A35947

R;Smith, L.A.; Schmidt, J.J.  
 Toxicol 28, 575-585, 1990

A;Title: Cloning and nucleotide sequences of crotoxin genes.

A;Reference number: A35947; MUID:90357261; PMID:2389256

A;Accession: A35947

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-65 <SMI>

C;Superfamily: crotoxin

Query Match 29.4%; Score 108; DB 2; Length 65;  
 Best Local Similarity 39.1%; Pred. No. 1.9e-05;  
 Matches 27; Conservative 9; Mismatches 21; Indels 12; Gaps 5;

Qy 1 MRHYLLFALLFLFVLPVPGH-GGIINTLQKYCRVGRGCAVLSCLPKEQIGK-STRG 56

Db 1 MKLYLLFALLFLFVLPVPGH-GGIINTLQKYCRVGRGCAVLSCLPKEQIGK-STRG 53

Qy 57 TRGRKCCRR 65

Db 54 WR-RKCCCK 61

#### RESULT 5

JCS324

A;Title: myotoxin a precursor - prairie rattlesnake

C;Species: Crotalus viridis viridis (prairie rattlesnake)

C;Date: 15-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 02-Jul-1998

C;Accession: JCS324

R;Norris, J.W.; Fry, R.M.; Tu, A.T.

Biochem. Biophys. Res. Commun. 230, 607-610, 1997

A;Title: The nucleotide sequence of the translated and untranslated regions of a cDNA for

A;Reference number: JCS324; MUID:97167753; PMID:9015371

A;Accession: JCS324

A;Molecule type: mRNA

A;Residues: 1-65 <NOR>

A;Experimental source: venom

A;Note: The authors translated the codon CAG for residue 27 as His and CRT for residue 4

C;Comment: This protein inhibits Ca2+ uptake into the sarcoplasmic reticulum by binding

C;Superfamily: crotoxin

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-64/Product: myotoxin a #status predicted <MAT>

Query Match 28.1%; Score 103; DB 2; Length 65;

Best Local Similarity 36.8%; Pred. No. 7.1e-05;

Matches 25; Conservative 11; Mismatches 22; Indels 10; Gaps 4;

Qy 1 MRHYLLFALLFLFVLPVPGH-GGIINTLQKYCRVGRGCAVLSCLPKEQIGK-STRG 58

Db 1 MKLYLLFALLFLFVLPVPGH-GGIINTLQKYCRVGRGCAVLSCLPKEQIGK-STRG 53

Qy 59 GR-KCCRR 65

Db 54 WKWKCCCK 61

#### RESULT 6

F45495

A;Title: beta-defensin-6 - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Feb-1994 #sequence\_revision 22-Apr-1995 #text\_change 25-Oct-1996

C;Accession: F45495

R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens

J. Biol. Chem. 268, 6641-6648, 1993

A;Title: Purification, primary structures, and antibacterial activities of beta-defensin

A;Reference number: A45495; MUID:93203284; PMID:8454635

A;Accession: F45495

A;Molecule type: protein

A;Residues: 1-42 <SEL>

A;Note: sequence modified after extraction from NCBI backbone

C;Keywords: antibacterial; disulfide bond; pyroglutamic acid

F;1-42/Product: beta-defensin-6 #status experimental <MAI>

F;1/Modified site: pyroglutamic acid (Gln) #status experimental

F;9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 24.3%; Score 89; DB 2; Length 42;

Best Local Similarity 48.5%; Pred. No. 0.002;

Matches 16; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 33 CRVGRGCAVLSCLPKEQIGK-STRGKCCRR 65

Db 9 CRVGRGCAVLSCLPKEQIGK-STRGKCCRR 41

#### RESULT 7

beta-defensin-3 - bovine  
 N;Alternate names: peptide BNBD-3  
 N;Contains: beta-defensin-2  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 24-Feb-1994 #sequence\_revision 22-Apr-1995 #text\_change 25-Oct-1996  
 C;Accession: C45495; B45495  
 R;Sequested, M.B.; Tang, Y.O.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens  
 J. Biol. Chem. 268, 6641-6648, 1993  
 A;Title: Purification, primary structures, and antibacterial activities of beta-defensin  
 A;Reference number: A45495; MUID:93203264; PMID:8454635  
 A;Accession: C45495  
 A;Molecule type: protein  
 A;Residues: 1-42 <SEL>  
 A;Note: sequence modified after extraction from NCBI backbone  
 A;Accession: B45495

A;Residues: 63-95 <SE2>  
A;Experimental source: peritoneal neutrophils  
R;Zhu, Q.; Solomon, S.  
Endocrinology 130, 1413-1423, 1992  
A;Title: Isolation and mode of action of rabbit corticostatic (antiadrenocorticotropin)  
A;Reference number: A49195; MUID:92164536; PMID:1311240  
A;Accession: B49195  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 63-95 <ZHU>  
A;Note: sequence extracted from NCBI backbone (NCBIP:85970)  
C;Comment: This peptide is active against some fungi and gram-positive bacteria in vitro  
C;Superfamily: mammalian defensin  
C;Keywords: antibacterial  
F;65-93,67-82,72-92/Disulfide bonds: #status predicted

Query Match 18.9%; Score 69.5; DB 1; Length 95;  
Best Local Similarity 48.3%; Pred. No. 0.68; 10; Indels 3; Gaps 1;  
Matches 14; Conservative 2; Mismatches 2; Mismatches 3; Gaps 1;

QY 40 CAVLSCLPKPEQIGKSTRGR---KCRR 65  
DB 67 CRRALCLPRRRAGFCRIRHPLCRR 95

RESULT 12  
G45495  
N;Alternate names: peptide BNB-7  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 24-Feb-1994 #sequence\_revision 22-Apr-1995 #text\_change 25-Oct-1996  
C;Accession: G45495  
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens  
J. Biol. Chem. 268, 6641-6648, 1993  
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin  
A;Reference number: A45495; MUID:93203284; PMID:8454635  
A;Accession: G45495  
A;Molecule type: protein  
A;Residues: 1-40 <SEL>  
A;Note: sequence modified after extraction from NCBI backbone  
C;Keywords: antibacterial; disulfide bond; pyroglutamic acid  
F;1-40/Product: beta-defensin-7 #status experimental <MAL>  
F;1/Modified site: pyroglutamic acid (Gln) #status experimental  
F;9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 18.8%; Score 69; DB 2; Length 40;  
Best Local Similarity 40.6%; Pred. No. 0.38; 17; Indels 0; Gaps 0;  
Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 33 CRVGRCAVLSCLPKPEQIGKSTRGRKCCR 64  
DB 9 CRNRGFCVPIRCFGRHRRQIGTCLGPRKCCR 40

RESULT 13  
I45495  
N;Alternate names: peptide BNB-9  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 24-Feb-1994 #sequence\_revision 22-Apr-1995 #text\_change 22-Apr-1995  
C;Accession: I45495; H45495  
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens  
J. Biol. Chem. 268, 6641-6648, 1993  
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin  
A;Reference number: A45495; MUID:93203264; PMID:8454635  
A;Accession: I45495  
A;Molecule type: protein  
A;Residues: 1-40 <SEL>  
A;Note: sequence modified after extraction from NCBI backbone  
A;Accession: H45495  
A;Residues: 3-40 <SE2>

A;Note: sequence extracted from NCBI backbone (NCBIP:127958)  
C;Keywords: pyroglutamic acid  
F;1-40/Product: beta-defensin-9 #status experimental <MAL>  
F;3-40/Product: beta-defensin-8 #status experimental <MA2>  
F;1/Modified site: pyroglutamic acid (Gln) #status experimental  
F;9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 18.8%; Score 69; DB 2; Length 40;  
Best Local Similarity 40.6%; Pred. No. 0.38; 17; Indels 0; Gaps 0;  
Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

QY 33 CRVGRCAVLSCLPKPEQIGKSTRGRKCCR 64  
DB 9 CRNRGFCVPIRCFGRHRRQIGTCLGPRKCCR 40

RESULT 14  
D47753  
N;Alternate names: peptide BNB-13  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 24-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 22-Apr-1995  
C;Accession: D47753; C47753  
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens  
J. Biol. Chem. 268, 6641-6648, 1993  
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin  
A;Reference number: A45495; MUID:93203264; PMID:8454635  
A;Accession: D47753  
A;Molecule type: protein  
A;Residues: 1-42 <SEL>  
A;Note: sequence extracted from NCBI backbone (NCBIP:127963)  
A;Accession: C47753  
A;Molecule type: protein  
A;Residues: 5-42 <SE2>  
A;Note: sequence extracted from NCBI backbone (NCBIP:127962)  
C;Keywords: disulfide bond  
F;1-42/Product: beta-defensin-13 #status experimental <MAL>  
F;5-42/Product: beta-defensin-12 #status experimental <MA2>  
F;9-38,16-31,21-39/Disulfide bonds: #status experimental

Query Match 18.5%; Score 68; DB 2; Length 42;  
Best Local Similarity 43.8%; Pred. No. 0.51; 17; Indels 0; Gaps 0;  
Matches 14; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 33 CRVGRCAVLSCLPKPEQIGKSTRGRKCCR 64  
DB 9 CGNRGVCVPIRCFGRHRRQIGTCLGPRKCCR 40

RESULT 15  
CXRSCH  
toxic peptide C - southern Pacific rattlesnake  
C;Species: Crotalus viridis helleri (southern Pacific rattlesnake)  
C;Date: 31-May-1979 #sequence\_revision 08-Oct-1981 #text\_change 23-Aug-1996  
C;Accession: A01737  
R;Maeda, N.; Tamiya, N.; Pattabhiraman, T.R.; Russell, P.E.  
Toxicol. 16, 431-441, 1978  
A;Title: Some chemical properties of the venom of the rattlesnake, Crotalus viridis helleri  
A;Reference number: A01737; MUID:79015339; PMID:694946  
A;Accession: A01737  
A;Molecule type: protein  
A;Residues: 1-43 <MAE>  
C;Superfamily: crotonine  
C;Keywords: myotoxin; venom  
F;4-36,11-30,18-37/Disulfide bonds: #status predicted

Query Match 18.1%; Score 66.5; DB 1; Length 43;  
Best Local Similarity 36.1%; Pred. No. 0.78; 15; Indels 3; Gaps 2;  
Matches 13; Conservative 5; Mismatches 15; Indels 3; Gaps 2;

QY 33 CRVGRGRC--AVLSCLPKPEQIGKSTRGR--KCRR 65  
DB 9 CRNRGFCVPIRCFGRHRRQIGTCLGPRKCCR 40



Db 4 CHKGGHCFPTVICLPPSSDFGMDCRWKKCKK 39

Search completed: October 31, 2003, 14:04:29  
Job time : 41 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2003, 13:55:57 ; Search time 23 Seconds  
(without alignments)  
136.991 Million cell updates/sec

Title: US-09-872-852-2

Perfect score: 367

Sequence: 1 MRHYLLFALLFLVVPFG.....KKEQIKCGRKRCRRKK 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	367	100.0	67	D103_HUMAN	P81534 homo sapien
2	133	36.2	64	D103_HUMAN	O15263 homo sapien
3	121.5	33.1	63	D103_MOUSE	O9W100 mus musculus
4	119	32.4	64	D101_PIG	O62697 sus scrofa
5	116	31.6	64	EAP_BOVIN	O02775 bos taurus
6	113	30.8	64	LAP_BOVIN	O28880 bos taurus
7	111	30.2	64	TAP_BOVIN	P25968 bos taurus
8	108	29.4	65	MYX1_CRODU	P24331 crotalus du
9	108	29.4	65	MYX3_CRODU	P24333 crotalus du
10	106	28.9	64	BD05_BOVIN	P46163 bos taurus
11	100.5	27.4	63	BD02_RAT	O88514 rattus norv
12	100	27.2	64	BD01_CAPIH	O97946 capra hircu
13	98	26.7	64	BD02_SHEEP	O19039 ovis aries
14	94	25.6	53	BD07_BOVIN	O18815 bos taurus
15	93	25.3	64	BD01_SHEEP	O19038 ovis aries
16	92	25.1	63	BD04_BOVIN	P46162 bos taurus
17	90.5	24.7	63	BD04_MOUSE	P82019 mus musculus
18	89	24.3	62	BD06_BOVIN	P46164 bos taurus
19	89	24.3	69	BD01_RAT	O89117 rattus norv
20	85	23.2	69	BD01_MOUSE	P56386 mus musculus
21	84	22.9	55	BD09_BOVIN	P46167 bos taurus
22	84	22.9	57	BD03_BOVIN	P46161 bos taurus
23	83.5	22.8	64	MYX2_CRODU	P24332 crotalus du
24	82.5	22.5	64	GLL3_CHICK	P46158 gallus gall
25	78.5	21.4	65	AMP1_MELGA	P80391 meleagris g
26	75	20.4	38	BD11_BOVIN	P46169 bos taurus
27	74	20.2	68	BD01_HUMAN	O09753 homo sapien
28	73.5	20.0	64	AMP2_MELGA	P80392 meleagris g
29	73.5	20.0	65	GLL1_CHICK	P46156 gallus gall
30	73.5	20.0	71	BD02_MOUSE	P82020 mus musculus
31	71	19.3	40	BD02_BOVIN	P46160 bos taurus
32	69.5	18.9	45	MYX_CRODU	P24330 crotalus ad
33	69.5	18.9	95	DEF3_RABIT	P01376 oryctolagus

34	69	18.8	38	1	BD08_BOVIN	P46166 bos taurus
35	69	18.8	40	1	BD07_BOVIN	P46165 bos taurus
36	68	18.5	38	1	BD12_BOVIN	P46170 bos taurus
37	68	18.5	42	1	BD13_BOVIN	P46171 bos taurus
38	66.5	18.1	43	1	MYX_CRODH	P01477 crotalus vi
39	66.5	18.1	65	1	D106_HUMAN	O8N104 homo sapien
40	66.5	18.1	73	1	D108_HUMAN	Q8N101 homo sapien
41	65.5	17.8	42	1	MYX4_CRODU	P01475 crotalus du
42	65.5	17.8	51	1	MYX4_CRODU	P24334 crotalus du
43	65.5	17.8	95	1	DEF4_RABIT	P01377 oryctolagus
44	65	17.7	68	1	BD01_MACMU	O18794 macaca mula
45	64	17.4	116	1	MCS_HUMAN	P49901 homo sapien

## ALIGNMENTS

RESULT 1					
D103_HUMAN					
ID	D103_HUMAN	STANDARD;	PRT;	67	AA.
AC	P81534; Q9NPF6;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Beta-defensin 3 precursor (BD-3) (hBD-3) (Beta-defensin 103) (Defensin DE like protein).				
GN	DEFB103 OR DEFB3 OR BD3.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
[1]	SEQUENCE FROM N.A., SEQUENCE OF 23-67, FUNCTION, TISSUE SPECIFICITY, INDUCTION, AND MASS SPECTROMETRY.				
RP	TISSUE=Keratinocytes, Lung epithelial cells, and Tracheal epithelium;				
RC	MEDLINE=21101950; PubMed=11085990;				
RX	"Isolation and characterization of human beta-defensin-3, a novel human inducible peptide antibiotic."				
RT	J. Biol. Chem. 276:5707-5713(2001).				
[2]	SEQUENCE FROM N.A., AND CHARACTERIZATION.				
RP	MEDLINE=21558153; PubMed=11702237;				
RX	Garcia J.-R., Jaumann F., Schulz S., Krause A., Rodriguez-Jimenez J., Forssmann U., Ademann K., Kluever E., Vogelmeier C., Becker D., Hedrich R., Forssmann W.-G., Bals R.,				
RA	"Identification of a novel, multifunctional beta-defensin (human beta-defensin 3) with specific antimicrobial activity. Its interaction with plasma membranes of Xenopus oocytes and the induction of macrophage chemotaxis."				
RT	Cell Tissue Res. 306:257-264(2001).				
[3]	SEQUENCE FROM N.A.				
RP	MEDLINE=21123260; PubMed=11223260;				
RX	Jia H.P., Schutte B.C., Schudy A., Linzmeier R., Guthmiller J.M., Johnson G.K., Tack B.F., Mitros J.P., Rosenthal A., Ganz T., McCray P.B. Jr.,				
RA	"Discovery of new human defensins using a genomics-based approach."				
RT	Gene 263:211-218(2001).				
[4]	SEQUENCE FROM N.A.				
RP	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.				
RA	Imai Y.;				
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.				
[5]	SEQUENCE FROM N.A.				
RP	Adler D.A., Whitmore G., Sheppard P., Holloway J., Presnell S., Jaspers S., Whitmore T., Fox B., Gosink J., Rixon M., Gao Z., Haldeman B., O'Hara P.;				
RA	"EST and genomic database mining yield novel human and mouse beta-defensins."				
RT	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.				
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.				
CC	!- FUNCTION: EXHIBITS ANTIMICROBIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIA S.AUREUS AND S.PYOGENES, GRAM-NEGATIVE BACTERIA				

P. AERUGINOSA AND E. COLI AND THE YEAST C. ALBICANS. KILLS  
MULTIRESTANT S. AUREUS AND VANCOMYCIN-RESISTENT E. FAECIUM. NO  
SIGNIFICANT HEMOLYTIC ACTIVITY WAS OBSERVED.  
-/- SUBCELLULAR LOCATION: Secreted.  
-/- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SKIN AND TONSILS, AND TO A  
LESSER EXTENT IN TRACHEA, UTERUS, KIDNEY, THYMUS, ADENOID, PHARYNX  
AND TONGUE. LOW EXPRESSION IN SALIVARY GLAND, BONE MARROW, COLON,  
STOMACH, POLYP AND LARYNX. NO EXPRESSION IN SMALL INTESTINE.  
-/- INDUCTION: BY INFECTION OF BACTERIA AND BY INTERFERON GAMMA.  
-/- MASS SPECTROMETRY: MW=5154.59; METHOD=Electrospray; RANGE=23-67.  
-/- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.  
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EMBL; AJ237673; CAC03097.1; -  
EMBL; AF295370; AAG02237.1; -  
EMBL; AF217245; AAF73853.1; -  
EMBL; AB037972; BAB40572.1; -  
EMBL; AF301470; AAG22030.1; -  
PDB; 1KJ6; 20-MAR-02.  
Genew; HGNC:15967; DEFB103.  
MIM; 606611; -  
GO; GO:0005576; C:extracellular; NAS.  
GO; GO:0008224; P:Gram-positive antibacterial peptide activity; TAS.  
GO; GO:0006965; P:anti-Gram-positive bacterial polypeptide in. . .; TAS.  
InterPro; IPR001855; Defensin\_beta.  
Pfam; PF00711; Defensin\_beta; 1.  
KW Antibiotic; Signal; 3D-structure.  
SIGNAL 1 22  
FT CHAIN 23 67 BETA-DEFENSIN 3.  
FT DISULFID 33 62 BY SIMILARITY.  
FT DISULFID 40 55 BY SIMILARITY.  
FT DISULFID 45 63 BY SIMILARITY.  
SQ SEQUENCE 67 AA; 7697 MW; 54266DE1C90D4B65 CRC64;  
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Query Match 100.0%; Score 367; DB 1; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.9e-35;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
-----  
Qy 1 MRHYLLFALLFLVFPVPGHGGIINTLQKYCRVGRGCAVLSCLPKERQIGKCSRGR 60  
Db 1 MRHYLLFALLFLVFPVPGHGGIINTLQKYCRVGRGCAVLSCLPKERQIGKCSRGR 60  
-----  
Qy 61 KCCRKK 67  
Db 61 KCCRKK 67  
-----  
RESULT 2  
BD02\_HUMAN STANDARD; PRT; 64 AA.  
ID BD02\_HUMAN  
AC O15263;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Beta-defensin 2 precursor (hbd-2) (Skin-antimicrobial peptide 1)  
(SAP1).  
GN DEFB4 OR DEFB2 OR DEFB102.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
TX MEDLINE=97345625; PubMed=9202117;  
Harder J., Bartels J.H., Christophers E., Schroeder J.-M.;  
TAS.

"A peptide antibiotic from human skin.";  
Nature 387:861-861(1997).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=99051334; PubMed=9831658;  
RA Liu L., Wang L., Jia H.P., Zhao C., Heng H.H.Q., Schutte B.C.,  
McCray P.B. Jr., Ganz T.;  
RA "Structure and mapping of the human beta-defensin HBD-2 gene and its  
expression at sites of inflammation.";  
RL Gene 222:237-244(1998).  
[3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20072673; PubMed=10603376;  
RA Diamond G., Kaiser V., Rhodes J., Russell J.P., Bevins C.L.;  
RA "Transcriptional regulation of beta-defensin gene expression in  
tracheal epithelial cells.";  
RL Infect. Immun. 68:113-119(2000).  
[4]  
RP SEQUENCE FROM N.A.  
RA Harder J., Schroeder J.M.;  
RT "Transcriptional regulation of the human beta-defensin-2 (hbd-2).";  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
[5]  
RP SYNTHESIS OF 24-64.  
RX MEDLINE=22007551; PubMed=12010514;  
RA Kluever E., Schulz A., Forssmann W.-G., Adermann K.;  
RT "Chemical synthesis of beta-defensins and LEAP-1/hepcidin.";  
RL J. Pept. Res. 59:241-248(2002).  
[6]  
RP X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).  
RX MEDLINE=20490730; PubMed=10906336;  
RA Hoover D.M., Rajashankar K.R., Blumenthal R., Puri A., Oppenheim J.J.,  
Chertov O., Lubkowski J.;  
RT "The structure of human beta-defensin-2 shows evidence of higher  
order oligomerization.";  
RL J. Biol. Chem. 275:32911-32918(2000).  
[7]  
RP STRUCTURE BY NMR OF 28-64.  
RX MEDLINE=21571984; PubMed=11714914;  
RA Bauer F., Schweimer K., Kluever E., Conejo-Garcia J.R.,  
Forssmann W.-G., Rosch P., Adermann K., Sticht H.;  
RT "Structure determination of human and murine beta-defensins reveals  
structural conservation in the absence of significant sequence  
similarity.";  
RL Protein Sci. 10:2470-2479(2001).  
CC -/- FUNCTION: HAS ANTIBACTERIAL ACTIVITY (POTENTIAL).  
CC -/- SUBCELLULAR LOCATION: Secreted.  
CC -/- TISSUE SPECIFICITY: EXPRESSED IN THE SKIN AND RESPIRATORY TRACT.  
CC -/- INDUCTION: By inflammation.  
CC -/- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP  
SUBFAMILY.  
-----  
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-----  
EMBL; Z71389; CAA95992.1; -  
EMBL; AF040153; AAC33549.1; -  
EMBL; AF071216; AAC69554.1; -  
EMBL; AJ000152; CAB65126.1; -  
PDB; 1FD3; 01-NOV-00.  
PDB; 1FD4; 01-NOV-00.  
PDB; 1EQ0; 26-NOV-01.  
PDB; 1FOQ; 31-DEC-02.  
Genew; HGNC:2767; DEFB4.  
MIM; 602215; -  
GO; GO:0006935; P:chemotaxis; TAS.  
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.

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DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0005613; P:response to pest/pathogen/parasite; TAS.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta.
DR SMART; SM00048; DEFSN; 1.
KW Antibiotic; Signal; 3D-structure.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 64 BETA-DEFENSIN 2.
FT DISULFID 31 60
FT DISULFID 38 53
FT DISULFID 43 61
FT STRAND 26 26
FT HELIX 28 33
FT TURN 34 35
FT STRAND 37 39
FT TURN 45 46
FT STRAND 48 52
FT TURN 56 57
FT STRAND 59 62
SQ SEQUENCE 64 AA; 7038 MW; 05D6454CE7ACD10E CRC64;

Query Match 36.2%; Score 133; DB 1; Length 64;
Best Local Similarity 42.4%; Pred. No. 1.1e-08;
Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

QY 1 MRIHYLLFALLFLFVPGVGGIINTLQKYYCRVGRCAVLSCLPKEEIGKSTGR 59
Db 1 MRVLYLLSFLPIFLPULPGVGGIGDPVT---CLKGAICHVPFCPRRYKQIGTCGUPG 57

QY 60 KRCRR 65
Db 58 TKCKK 63

RESULT 3
BD03 MOUSE
ID BD03 MOUSE STANDARD; PRT; 63 AA.
AC Q9WTLO.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-defensin 3 precursor (BD-3) (mBD-3).
GN DEB3 OR BD3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, INDUCTION; AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6; TISSUE=Lung;
RX MEDLINE=99307216; PubMed=10377137;
RA Bals R., Wang X., Meegalla R.L., Wattler S., Weiner D.J., Nehls M.C.,
RT Wilson J.M.;
RT "Mouse beta-defensin 3 is an inducible antimicrobial peptide expressed
in the epithelia of multiple organs.";
RL Infect. Immun. 67:3542-3547(1999).
RN [2]
RP TISSUE SPECIFICITY.
RC STRAIN=C57BL/6, 129/SvJ, and FVB; TISSUE=Lung;
RX MEDLINE=20517883; PubMed=10922379;
RA Jia H.P., Wolk S.A., Schutte B.C., Lee S.K., Vivado A., Tack B.F.,
RA Bevins C.L., McCray P.B. Jr.;
RT "A novel murine beta-defensin expressed in tongue, esophagus, and
trachea.";
RL J. Biol. Chem. 275:33314-33320(2000).
CC -!- FUNCTION: ANTIMICROBIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIA
CC E. COLI AND P. AERUGINOSA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SALIVARY GLANDS,
EPIDIDYMIS, OVARY AND PANCREAS AND TO A LESSER EXTENT IN LUNG,
LIVER AND BRAIN. LOW OR NO EXPRESSION IN SKELETAL MUSCLE AND
TONGUE.
CC

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CC -!- INDUCTION: BY bacterial infection.
CC -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
CC SUBFAMILY.
CC
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CC
DR EMBL; AF093245; AAD29573.1; -.
DR EMBL; AF092929; AAD29572.1; -.
DR HSP; P46170; 1BNB.
DR MGD; MGI:1351612; Defb3.
DR InterPro; IPR001855; Defensin_beta.
DR InterPro; IPR006080; Defensin_mammal.
DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00048; DEFSN; 1.
KW Antibiotic; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 22 POTENTIAL.
FT CHAIN 23 63 BETA-DEFENSIN 3.
FT DISULFID 31 59 BY SIMILARITY.
FT DISULFID 38 52 BY SIMILARITY.
FT DISULFID 42 60 BY SIMILARITY.
SQ SEQUENCE 63 AA; 7126 MW; 9D59BC8AD16EA330 CRC64;

Query Match 33.1%; Score 121.5; DB 1; Length 63;
Best Local Similarity 43.9%; Pred. No. 2.2e-07;
Matches 29; Conservative 4; Mismatches 30; Indels 3; Gaps 2;

QY 1 MRIHYLLFALLFLFVPGVGGIINTLQKYYCRVGRCAVLSCLPKEEIGKSTGR 60
Db 1 MRIHYLLFALLFLFVPGVGGIINTLQKYYCRVGRCAVLSCLPKEEIGKSTGR 57

QY 61 KCCRRK 66
Db 58 KCCRRK 63

RESULT 4
BD01 PIG
ID BD01 PIG STANDARD; PRT; 64 AA.
AC O62897;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-defensin 1 precursor (BD-1) (Defensin, beta 1).
GN DEB1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98196859; PubMed=9537511;
RA Zhang G., Wu H., Shi J., Ganz T., Ross C., Blecha F.;
RT "Molecular cloning and tissue expression of porcine beta-defensin-1.";
RL FEBS Lett. 424:37-40(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99377035; PubMed=10446172;
RA Zhang G., Hiraiwa H., Yasue H., Wu H., Ross C.R., Troyer D.,
RA Blecha F.;
RT "Cloning and characterization of the gene for a new epithelial
beta-defensin. Genomic structure, chromosomal localization, and
evidence for its constitutive expression.";
RL J. Biol. Chem. 274:24031-24037(1999).
CC -!- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC

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DR EMBL; AF031666; AAC39175.1; -  
 DR EMBL; AF132038; AAD51137.1; -  
 DR HSP; P46170; 1BNB.  
 DR InterPro; IPR001855; Defensin\_beta.  
 DR InterPro; IPR006080; Defensin\_mammal.  
 DR Pfam; PF00711; Defensin\_beta; 1.  
 DR SMART; SM00048; DEFSN; 1.  
 KW Antibiotic; Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT PROPEP 21 23 BY SIMILARITY.  
 FT CHAIN 24 64 BETA-DEFENSIN 1.  
 FT DISULFID 31 60 BY SIMILARITY.  
 FT DISULFID 38 53 BY SIMILARITY.  
 FT DISULFID 43 61 BY SIMILARITY.  
 SQ SEQUENCE 64 AA; 7066 MW; 0A4B7494BA3E337A CRC64;

Query Match 32.4%; Score 119; DB 1; Length 64;  
 Best Local Similarity 40.9%; Pred. No. 4.3e-07;  
 Matches 27; Conservative 6; Mismatches 31; Indels 2; Gaps 1;

QY 1 MRIHYLLPALLFLVVPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKBEQIGKSTRGR 60  
 DB 1 MRLHLLVLLVLLVLPVGL--LKNIGNSVSLNRKGVCMGPKAPKMQIGTCGMPQV 58  
 QY 61 KCCRRK 66  
 DB 59 KCCRRK 64

## RESULT 5

EAP\_BOVIN  
 ID\_EAP\_BOVIN STANDARD; PRT; 64 AA.  
 AC 002775;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Enteric beta-defensin precursor.  
 GN BBD.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP MEDLINE=98147718; PubMed=9489394;  
 RA Tarver A.P., Clark D.P., Diamond G., Russell J.P.,  
 RA Brdjmunt-Bromage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,  
 RA Wines M., Wang S., Bevins C.L.;  
 RT "Enteric beta-defensin; molecular cloning and characterization of a  
 RT gene with inducible intestinal epithelial cell expression associated  
 RT with Cryptosporidium parvum infection.";  
 RL Infect. Immun. 66:1045-1056(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96014297; PubMed=8589529;  
 RA Gallagher D.S. Jr., Ryan A.M., Diamond G., Bevins C.L., Womack J.E.;  
 RT "Somatic cell mapping of beta-defensin genes to cattle syntenic group  
 RT U25 and fluorescence in situ localization to chromosome 27.";  
 RL Mamm. Genome 6:554-556(1995).  
 CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: INDUCIBLY EXPRESSED IN ENTERIC EPITHELIAL  
 CC CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP

## SUBFAMILY.

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DR EMBL; AF000362; AAC48805.1; -  
 DR EMBL; AF016539; AAC48804.1; -  
 DR HSP; P46170; 1BNB.  
 DR InterPro; IPR001855; Defensin\_beta.  
 DR InterPro; IPR006080; Defensin\_mammal.  
 DR Pfam; PF00711; Defensin\_beta; 1.  
 DR SMART; SM00048; DEFSN; 1.  
 KW Antibiotic; Signal.  
 FT SIGNAL 1 26 BY SIMILARITY.  
 FT CHAIN 27 64 ENTERIC BETA-DEFENSIN.  
 FT DISULFID 31 60 BY SIMILARITY.  
 FT DISULFID 38 53 BY SIMILARITY.  
 FT DISULFID 43 61 BY SIMILARITY.  
 SQ SEQUENCE 64 AA; 7126 MW; 7B8642AE6F7A6068 CRC64;

Query Match 31.6%; Score 116; DB 1; Length 64;  
 Best Local Similarity 44.6%; Pred. No. 9.4e-07;  
 Matches 29; Conservative 4; Mismatches 28; Indels 4; Gaps 2;

QY 1 MRIHYLLPALLFLVVPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKBEQIGKSTRGR 59  
 DB 1 MRLHLLVLLVLLVLPVGL--LKNIGNSVSLNRKGVCMGPKAPKMQIGTCGMPQV 57  
 QY 60 KCCRRK 64  
 DB 58 KCCRRK 62

## RESULT 6

LAP\_BOVIN  
 ID\_LAP\_BOVIN STANDARD; PRT; 64 AA.  
 AC Q28880; Q28202;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Lingual antimicrobial peptide precursor.  
 GN LAP.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Tongue epithelium;  
 RX MEDLINE=95192714; PubMed=7886453;  
 RA Schonwetter B.S., Stolzenberg E.D., Zasloff M.A.;  
 RT "Epithelial antibiotics induced at sites of inflammation.";  
 RL Science 267:1645-1648(1995).  
 RN [2]  
 RP SEQUENCE OF 3-64 FROM N.A.  
 RX MEDLINE=96201562; PubMed=8613361;  
 RA Russell J.P., Diamond G., Tarver A.P., Scanlin T.F., Bevins C.L.;  
 RT "Coordinate induction of two antibiotic genes in tracheal epithelial  
 RT cells exposed to the inflammatory mediators lipopolysaccharide and  
 RT tumor necrosis factor alpha.";  
 RL Infect. Immun. 64:1565-1568(1996).  
 CC -1- FUNCTION: SHOWS A BROAD SPECTRUM OF ANTIBACTERIAL AND ANTIFUNGAL  
 CC ACTIVITIES.  
 CC -1- TISSUE SPECIFICITY: IN MANY OF THE EXPOSED EPITHELIAL SURFACES  
 CC INCLUDING CONJUNCTIVAE, BRONCHI, COLON, URINARY TRACT AND TRACHEA.  
 CC -1- DEVELOPMENTAL STAGE: NOT FOUND IN FETUS.  
 CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP

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CC -----
CC EMBL; S76279; AAB33727.1; -.
CC EMBL; U48357; AAB05401.1; -.
CC PIR; A56128; A56128.
CC HSSP; P46170; 1BNB.
CC InterPro; IPR001855; Defensin_beta.
CC InterPro; IPR006080; Defensin_mammal.
CC Pfam; PF00711; Defensin_beta; 1.
CC SMART; SM00048; DEFSN; 1.
CC Antibiotic; Signal; Fungicide.
CC SIGNAL 1 19
CC PEPTIDE 20 64 LINGUAL ANTIMICROBIAL PEPTIDE.
CC DISULFID 31 60 BY SIMILARITY.
CC DISULFID 38 53 BY SIMILARITY.
CC DISULFID 43 61 BY SIMILARITY.
CC CONFLICT 20 20 G -> R (IN REF. 2).
CC SEQUENCE 64 AA; 7041 MW; BD24CDA3B3912F8F CRC64.
CC -----
CC Query Match 30.8%; Score 113; DB 1; Length 64;
CC Best Local Similarity 42.4%; Pred. No. 2.1e-06;
CC Matches 28; Conservative 3; Mismatches 33; Indels 1; Gaps 1;
CC
CC QY 1 MRIHYLLFALLFLVFPVGHGIIINTLQKYYCVRGRCVAVLSCLPKKEQIGKCSYGR 60
CC DB 1 MRLHLLALLFLVLL--SAGSGTQGVNSQSCRRNKGCIVPCRCPSMRQIGTCLGAQV 58
CC
CC QY 61 KCCRK 66
CC DB 59 KCCRK 64
CC
CC RESULT 7
CC TAP BOVIN STANDARD; PRT; 64 AA.
CC AC P25068; O97532;
CC DT 01-MAY-1992 (Rel. 22, Created)
CC DT 01-MAY-1992 (Rel. 22, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Tracheal antimicrobial peptide precursor (TAP).
CC OS Bos taurus (Bovine).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC OC Bovidae; Eutheria; Bos.
CC OX NCBI_TaxID=9913;
CC [1]
CC SEQUENCE FROM N.A., AND SEQUENCE OF 27-59.
CC RC TISSUE=Tracheal epithelium;
CC RX MEDLINE=91219490; PubMed=2023943;
CC RA Diamond G., Zaslloff M., Eck H., Brasseur M., Maloy W.L., Bevins C.L.;
CC "Tracheal antimicrobial peptide, a cysteine-rich peptide from
CC mammalian tracheal mucosa: peptide isolation and cloning of a cDNA.";
CC Proc. Natl. Acad. Sci. U.S.A. 88:3952-3956(1991).
CC [2]
CC SEQUENCE FROM N.A.
CC RC TISSUE=Trachea;
CC RX MEDLINE=93281626; PubMed=8506305;
CC RA Diamond G., Jones D.E., Bevins C.L.;
CC "Airway epithelial cells are the site of expression of a mammalian
CC antimicrobial peptide gene.";
CC Proc. Natl. Acad. Sci. U.S.A. 90:4596-4600(1993).
CC [3]
CC SEQUENCE FROM N.A.
CC RA Ryan L.K., Rhodes J., Bhat M., Diamond G.;
CC Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

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CC
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY IN VITRO AGAINST ESCHERICHIA
CC COLI, STAPHYLOCOCCUS AUREUS, KLEBSIELLA PNEUMONIA, AND PSEUDOMONAS
CC AERUGINOSA. IN ADDITION, THE PEPTIDE IS ACTIVE AGAINST CANDIDA
CC ALBICANS, INDICATING A BROAD SPECTRUM OF ACTIVITY.
CC -!- TISSUE SPECIFICITY: TRACHEAL EPITHELIUM.
CC -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
CC SUBFAMILY.
CC -----
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CC -----
CC EMBL; M63023; AAB61757.1; -.
CC EMBL; L13373; AAA72363.1; -.
CC EMBL; AF014106; AAD01521.1; -.
CC PIR; A47438; A47438.
CC HSSP; P46170; 1BNB.
CC InterPro; IPR001855; Defensin_beta.
CC InterPro; IPR006080; Defensin_mammal.
CC Pfam; PF00711; Defensin_beta; 1.
CC SMART; SM00048; DEFSN; 1.
CC Antibiotic; Signal.
CC SIGNAL 1 26
CC CHAIN 27 64 TRACHEAL ANTIMICROBIAL PEPTIDE.
CC DISULFID 31 60 BY SIMILARITY.
CC DISULFID 38 53 BY SIMILARITY.
CC DISULFID 43 61 BY SIMILARITY.
CC CONFLICT 18 18 W -> S (IN REF. 3).
CC CONFLICT 46 46 S -> N (IN REF. 3).
CC SEQUENCE 64 AA; 6953 MW; 58617B95E02918E6 CRC64;
CC -----
CC Query Match 30.2%; Score 111; DB 1; Length 64;
CC Best Local Similarity 41.8%; Pred. No. 3.5e-06;
CC Matches 28; Conservative 7; Mismatches 28; Indels 4; Gaps 2;
CC
CC QY 1 MRIHYLLFALLFLVFPVGHGIIINTLQKYYCVRGRCVAVLSCLPKKEQIGKCSYGR 59
CC DB 1 MRLHLLALLFLVLSAWSGFTQGVNPS---CVRNKGICVPIRCPSMRQIGTCLGVA 57
CC
CC QY 60 KCCRK 66
CC DB 58 KCCRK 64
CC
CC RESULT 8
CC MYX1 CRODU STANDARD; PRT; 65 AA.
CC ID MYX1 CRODU STANDARD; PRT; 65 AA.
CC AC P24331;
CC DT 01-MAR-1992 (Rel. 21, Created)
CC DT 01-MAR-1992 (Rel. 21, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Myotoxin 1 precursor (Crotamine 1).
CC OS Crocotalus durissus terrificus (South American rattlesnake).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Lepidodactylia; Squamata; Scieroglossa; Serpentes; Colubroidea;
CC OC Viperidae; Crotalinae; Crotalus.
CC OX NCBI_TaxID=8732;
CC [1]
CC SEQUENCE FROM N.A.
CC RC TISSUE=Venom gland;
CC RX MEDLINE=90357261; PubMed=2389256;
CC RA Smith L.A., Schmidt J.J.;
CC "Cloning and nucleotide sequences of crotamine genes.";
CC Toxicon 28:575-585(1990).
CC -!- FUNCTION: Causes severe muscle necrosis by a non-enzymatic
CC mechanism. Acts extremely rapidly and serves two primary
CC functions: limit the flight of prey by causing instantaneous
CC paralysis of the hind limbs and promote rapid death by paralysis
CC of the diaphragm.

```

CC -1- SIMILARITY: BELONGS TO THE MYOTOXIN FAMILY OF SNAKE TOXINS.

DR PIR: A35947; A35947.

DR InterPro: IPR000881; Myotoxin.

DR Pfam: PF00819; Myotoxins; 1.

DR ProDom: PD005972; Myotoxin; 1.

DR PROSITE: PS00459; MYOTOXINS; 1.

KW Toxin; Signal.

FT SIGNAL 1 22

FT CHAIN 23 64 MYOTOXIN 1.

FT DISULFID 26 58 BY SIMILARITY.

FT DISULFID 33 52 BY SIMILARITY.

FT DISULFID 40 59 BY SIMILARITY.

FT SEQUENCE 65 AA; 7443 MW; A1B75A6CC7359806 CRC64;

Query Match 29.4%; Score 108; DB 1; Length 65;

Best Local Similarity 39.1%; Pred. No. 7.9e-06;

Matches 27; Conservative 9; Mismatches 21; Indels 12; Gaps 5;

OY 1 MRIHYLLFALLFLFVPPVPGHGGIINTLQKYCRVGRGCAVLS--CLPKEEQIGK--CS 56

DB 1 MKIYLLFAFLFLAFLSEFG-----NAYKR--CHIKGGHCFPGKICIPSSDFGKMDCP 53

OY 57 TRGRKCCRR 65

DB 54 WR-RKCKCK 61

RESULT 9

ID MYX3\_CRODU STANDARD; PRT; 65 AA.

AC P24333;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Myotoxin 3 precursor (Crotamine 3).

OS Crotalus durissus terrificus (South American rattlesnake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lipidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Crotalus.

OX NCBI\_TaxID=8732;

RN SEQUENCE FROM N.A.

RP TISSUE=Venom gland;

RC MEDLINE=90357261; PubMed=2389256;

RA Smith L.A., Schmidt J.J.;

RT Cloning and nucleotide sequences of crotamine genes.;

RL Toxin 28:575-585(1990).

CC -1- FUNCTION: Causes severe muscle necrosis by a non-enzymatic

mechanism. Acts extremely rapidly and serves two primary

functions: limit the flight of prey by causing instantaneous

paralysis of the hind limbs and promote rapid death by paralysis

of the diaphragm.

CC -1- SIMILARITY: BELONGS TO THE MYOTOXIN FAMILY OF SNAKE TOXINS.

DR PIR: C35947; C35947.

DR InterPro: IPR000881; Myotoxin.

DR Pfam: PF00819; Myotoxins; 1.

DR ProDom: PD005972; Myotoxin; 1.

DR PROSITE: PS00459; MYOTOXINS; 1.

KW Toxin; Signal.

FT SIGNAL 1 22

FT CHAIN 23 64 MYOTOXIN 1.

FT DISULFID 26 58 BY SIMILARITY.

FT DISULFID 33 52 BY SIMILARITY.

FT DISULFID 40 59 BY SIMILARITY.

FT SEQUENCE 65 AA; 7371 MW; A1B75A6CC515BA06 CRC64;

Query Match 29.4%; Score 108; DB 1; Length 65;

Best Local Similarity 39.1%; Pred. No. 7.9e-06;

Matches 27; Conservative 9; Mismatches 21; Indels 12; Gaps 5;

OY 1 MRIHYLLFALLFLFVPPVPGHGGIINTLQKYCRVGRGCAVLS--CLPKEEQIGK--CS 56

DB 1 MKIYLLFAFLFLAFLSEFG-----NAYKR--CHIKGGHCFPGKICIPSSDFGKMDCP 53

OY 57 TRGRKCCRR 65

DB 54 WR-RKCKCK 61

RESULT 9

ID MYX3\_CRODU STANDARD; PRT; 65 AA.

AC P24333;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Myotoxin 3 precursor (Crotamine 3).

OS Crotalus durissus terrificus (South American rattlesnake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lipidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Crotalus.

OX NCBI\_TaxID=8732;

RN SEQUENCE FROM N.A.

RP TISSUE=Venom gland;

RC MEDLINE=90357261; PubMed=2389256;

RA Smith L.A., Schmidt J.J.;

RT Cloning and nucleotide sequences of crotamine genes.;

RL Toxin 28:575-585(1990).

CC -1- FUNCTION: Causes severe muscle necrosis by a non-enzymatic

mechanism. Acts extremely rapidly and serves two primary

functions: limit the flight of prey by causing instantaneous

paralysis of the hind limbs and promote rapid death by paralysis

of the diaphragm.

CC -1- SIMILARITY: BELONGS TO THE MYOTOXIN FAMILY OF SNAKE TOXINS.

DR PIR: C35947; C35947.

DR InterPro: IPR000881; Myotoxin.

OY 57 TRGRKCCRR 65

DB 54 WR-RKCKCK 61

RESULT 10

ID BD05\_BOVIN STANDARD; PRT; 64 AA.

AC P46163; O97533;

DT 01-NOV-1995 (Rel. 32, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Beta-defensin 5 precursor (BNDB-5).

OC Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN SEQUENCE FROM N.A.

RP Kurts B., Pitra C., Schwerin M., Seyfert H.-M.;

RT "Beta defensin-encoding genes are selected for divergent sequences of

the mature anti-bacterial peptide.;"

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE OF 1-54 FROM N.A., AND TISSUE SPECIFICITY.

RC TISSUE=Alveolar macrophage;

RA MEDLINE=98114406; PubMed=9453661;

RX Ryan L.K., Rhodes J., Bhat M., Diamond G.;

RT "Expression of beta-defensin genes in bovine alveolar macrophages.;"

RL Infect. Immun. 66:878-881(1998).

RN SEQUENCE OF 23-64, FUNCTION AND TISSUE SPECIFICITY.

RC STRAIN=Hereford; TISSUE=Neutrophils;

RA MEDLINE=93203284; PubMed=8454635;

RX Selsted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,

RA Smith W., Henschen A.H., Cullor J.S.;

RT "Purification, primary structures, and antibacterial activities of

beta-defensins, a new family of antimicrobial peptides from bovine

neutrophils.;"

RL J. Biol. Chem. 268:6641-6648(1993).

RN REVISIONS TO C-TERMINUS.

RA Selsted M.E.;

RL Submitted (MAY-1996) to the SWISS-PROT data bank.

CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY. ACTIVE AGAINST E. COLI ML35

BUT NOT AGAINST S. AUREUS 502A.

CC -1- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES. ALVEOLAR MACROPHAGES.

CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.

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CC EMBL; AJ278799; CAC15400.1; -

DR EMBL; AF014108; AAD01523.1; -

DR HSSP; P46170; 1BNE.

DR InterPro: IPR001855; Defensin\_beta.

DR InterPro: IPR006080; Defensin\_mammal.

DR Pfam; PF00711; Defensin\_beta; 1.

DR SMART; SM00048; DEFSN; 1.

KW Antibiotic; Signal; Pyrrolidone carboxylic acid.

FT SIGNAL 1 22

FT CHAIN 23 64 BETA-DEFENSIN 5.

FT MOD\_RES 23 23 PYRROLIDONE CARBOXYLIC ACID.

FT DISULFID 31 60 BY SIMILARITY.

FT DISULFID 38 53 BY SIMILARITY.

```
FT DISULPID 43 61 BY SIMILARITY.
FT CONFLICT 54 54 F -> S (IN REF. 2).
SQ SEQUENCE 64 AA; 7228 MW; 125A5278709131FC CRC64;

Query Match 28.9%; Score 106; DB 1; Length 64;
Best Local Similarity 40.0%; Pred. No. 1.3e-05;
Matches 26; Conservative 5; Mismatches 32; Indels 2; Gaps 1;

QY 1 MRIHYLLFALLFLVLPVPGHGIINTLQKYYCRVGRGRCVAVLSCLPKBEQIGKCGTRGR 60
Db 1 MRLHLLLVLLFLVLSAGSGFTQWRNPQS--CRWNGVCIPISCPGNMRQIGTCGPRV 58
QY 61 KCCR 65
Db 59 PCCR 63

RESULT 11
BD02_RAT
ID BD02_RAT STANDARD; PRT; 63 AA.
AC O88514;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-defensin 2 precursor (BD-2) (RBD-2).
GN DEFB2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wiistar;
RX MEDLINE=93386883; PubMed=10456937;
RA Jia H.P., Mills J.N., Barahmand-Pour P., Nishimura D.,
RA Mallampalli R.K., Wang G., Wiles K., Tack B.F., Bevins C.L.,
RA McCray P.B. Jr.;
RT "Molecular cloning and characterization of rat genes encoding
RT homologues of human beta-defensins."
RL Infect. Immun. 67:4827-4833(1999).
CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Highly expressed in lung.
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
CC SUBFAMILY.
-----
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-----
EMBL; AF068861; AAC28072.1; -
HSSP; O15263; IPD3.
DR InterPro; IPR001855; Defensin beta.
DR InterPro; IPR006080; Defensin mammal.
DR Pfam; PF00711; Defensin_beta_1.
DR SMART; SM00048; DEFSN; 1.
KW Antibiotic; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 7 POTENTIAL.
FT CHAIN 22 63 BETA-DEFENSIN 2.
FT DISULPID 31 59 BY SIMILARITY.
FT DISULPID 38 52 BY SIMILARITY.
FT DISULPID 42 60 BY SIMILARITY.
SQ SEQUENCE 63 AA; 6946 MW; 826099DE2144ACF4 CRC64;

Query Match 27.4%; Score 100.5; DB 1; Length 63;
Best Local Similarity 37.9%; Pred. No. 5.5e-05;
Matches 25; Conservative 7; Mismatches 31; Indels 3; Gaps 2;
```

```
QY 1 MRIHYLLFALLFLVLPVPGHGIINTLQKYYCRVGRGRCVAVLSCLPKBEQIGKCGTRGR 60
Db 1 MRIHYLLFALLFLVLSPLASFTQSIN--NPITCLTKGGVCMG-PCTGGPRQIGTCGCPRV 57
QY 61 KCCR 66
Db 59 RCCR 63

RESULT 12
BD01_CAPI
ID BD01_CAPI STANDARD; PRT; 64 AA.
AC O97946;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Beta-defensin 1 precursor (BD-1).
GN DEFB1.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RA Zhao C., Nguyen T., Lehrer R.I.;
RT "Molecular cloning and tissue expression of goat b-defensin-1."
RL Submitted (JUN-1998) to the EMBL/Genbank/DDAJ databases.
CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
-----
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-----
EMBL; Y17679; CAAT6811.1; -
HSSP; P46170; IBNB.
DR InterPro; IPR001855; Defensin beta.
DR InterPro; IPR006080; Defensin mammal.
DR Pfam; PF00711; Defensin_beta_1.
DR SMART; SM00048; DEFSN; 1.
KW Antibiotic; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 26 POTENTIAL.
FT CHAIN 27 64 BETA-DEFENSIN 1.
FT DISULPID 31 60 BY SIMILARITY.
FT DISULPID 38 53 BY SIMILARITY.
FT DISULPID 43 61 BY SIMILARITY.
SQ SEQUENCE 64 AA; 7258 MW; 492B824C8F578042 CRC64;

Query Match 27.2%; Score 100; DB 1; Length 64;
Best Local Similarity 37.9%; Pred. No. 6.4e-05;
Matches 25; Conservative 5; Mismatches 34; Indels 2; Gaps 1;

QY 1 MRIHYLLFALLFLVLPVPGHGIINTLQKYYCRVGRGRCVAVLSCLPKBEQIGKCGTRGR 60
Db 1 MRLHLLLVLLFLVLSAGSGFTQWRNPQS--SAGSGFTQIRSRNRKNGVCAUTCRPNRQIGTCGPRV 58
QY 61 KCCR 66
Db 59 KCCR 64

RESULT 13
BD02_SHEEP
ID BD02_SHEEP STANDARD; PRT; 64 AA.
AC O19039;
```



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DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-defensin 2 precursor (BD-2) (sBD2).
GN DEF2 OR BD2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98138497; PubMed=9478010;
RA Huttner K.M., Brezinski-Caliguri D.J., Mahoney M.M., Diamond G.;
RT "Antimicrobial peptide expression is developmentally regulated in the
RT ovine gastrointestinal tract.";
RL J. Nutr. 128:297S-299S(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98121317; PubMed=9461419;
RA Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
RT "Localization and genomic organization of sheep antimicrobial peptides
RT genes.";
RL Gene 206:85-91(1998).
CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U75251; AAB61996.1; --
CC HSP; P46170; 1BNB.
CC InterPro; IPR001855; Defensin_beta.
CC InterPro; IPR006080; Defensin_mammal.
CC Pfam; PF00711; Defensin_beta; 1.
CC SMART; SM00048; DEFSN; 1.
CC KW Antibiotic; Signal.
CC FT SIGNAL 1 22 BY SIMILARITY.
CC FT CHAIN 23 64 BETA-DEFENSIN 2.
CC FT DISULFID 31 60 BY SIMILARITY.
CC FT DISULFID 38 53 BY SIMILARITY.
CC FT DISULFID 43 61 BY SIMILARITY.
CC SQ SEQUENCE 64 AA; 7078 MW; C744942B364716C0 CRC64;

Query Match 26.7%; Score 98; DB 1; Length 64;
Best Local Similarity 37.3%; Pred. No. 0.00011;
Matches 25; Conservative 8; Mismatches 30; Indels 4; Gaps 2;

QY 1 MRHLLVLLFLVLPVPGH-GGIINTLQKYYCVRGRCNVLSCPLKPEIQKCKSTRG 59
DB 1 MRHLLVLLVFFVLSAGSGFTGVTDSLS---CRWKKGICVLTRCPGTRQIGTCFGPP 57
QY 60 RKCCRRK 66
DB 58 VKCRLK 64

RESULT 14
BDC7 BOVIN
ID BDC7 BOVIN STANDARD; PRT; 53 AA.
AC O18815;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Beta-defensin C7 precursor (BBD (C7)) (Fragment).
OS Bos taurus (Bovine).

```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98147718; PubMed=9488394;
RA Tarver A.P., Clark D.P., Diamond G., Russell J.P.,
RA Erdjument-Bromage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,
RA Wines M., Hwang S., Bevins C.L.;
RT "Enteric beta-defensin: molecular cloning and characterization of a
RT gene with inducible intestinal epithelial cell expression associated
RT with Cryptosporidium parvum infection.";
RL Infect. Immun. 66:1045-1056(1998).
CC -1- FUNCTION: HAS BACTERICIDAL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF016395; AAC48802.1; --
CC HSP; P46170; 1BNB.
CC InterPro; IPR001855; Defensin_beta.
CC InterPro; IPR006080; Defensin_mammal.
CC Pfam; PF00711; Defensin_beta; 1.
CC SMART; SM00048; DEFSN; 1.
CC KW Antibiotic; Signal.
CC FT SIGNAL 1 1 ? POTENTIAL.
CC FT PROPEP 1 15 POTENTIAL.
CC FT CHAIN 16 53 BETA-DEFENSIN C7.
CC FT DISULFID 20 49 BY SIMILARITY.
CC FT DISULFID 27 42 BY SIMILARITY.
CC FT DISULFID 32 50 BY SIMILARITY.
CC SQ SEQUENCE 53 AA; 5650 MW; 34659DF3A0489F4A CRC64;

Query Match 25.6%; Score 94; DB 1; Length 53;
Best Local Similarity 41.1%; Pred. No. 0.00026;
Matches 23; Conservative 5; Mismatches 22; Indels 6; Gaps 1;

QY 9 ALLFLFLVPPVPGHGGIINTLQKYYCVRGRCNVLSCPLKPEIQKCKSTRGKCCR 64
DB 2 ALLFLVLSAGSGISGPLS-----CRKKGICILIRCPGPMRQIGTCFGRPVKCCR 51

RESULT 15
BDC1 SHEEP
ID BDC1 SHEEP STANDARD; PRT; 64 AA.
AC O19038;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-defensin 1 precursor (BD-1) (sBD1).
GN DEFB1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98138497; PubMed=9478010;
RA Huttner K.M., Brezinski-Caliguri D.J., Mahoney M.M., Diamond G.;
RT "Antimicrobial peptide expression is developmentally regulated in the
RT ovine gastrointestinal tract.";
RL J. Nutr. 128:297S-299S(1998).

```

Search completed: October 31, 2003, 14:02:00  
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: October 31, 2003, 13:59:07 ; Search time 95 Seconds  
(without alignments)  
181.995 Million cell updates/sec

Title: US-09-872-852-2

Perfect score: 367

Sequence: 1 MRIHYLLFALLFLVLPVPG.....KEEQIGKSTRGKCRKK 67

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	355	96.7	67	Q8NFG6	Q8nfg6 homo sapien
2	349	95.1	64	Q95JD2	Q95jd2 pan troglod
3	135	36.8	64	Q9TT12	Q9tt12 pan troglod
4	134	36.5	64	Q9BDS9	Q9bds9 macaca mula
5	105	28.6	64	Q97942	Q97942 capra hircu
6	105	28.6	65	Q9PWF3	Q9pwf3 crotalus du
7	103	28.1	65	Q57540	Q57540 crotalus du
8	102	27.8	71	Q91V70	Q91v70 mus musculu
9	99	27.0	64	Q9EPV9	Q9epv9 mus musculu
10	98.5	26.8	63	Q91VD6	Q91vd6 mus musculu
11	96.5	26.3	80	Q9DG58	Q9dg58 gallus gall
12	96	26.2	64	Q73799	Q73799 crotalus du
13	93	25.3	60	Q8R556	Q8r556 mus musculu
14	92	25.1	60	Q91V82	Q91v82 mus musculu
15	89.5	24.4	59	Q9DG57	Q9dg57 meleagris g
16	82.5	22.5	64	Q8R214	Q8r214 mus musculu

17	79.5	21.7	67	11	Q8R216
18	78	21.3	80	6	Q9MZ26
19	76	20.7	80	4	Q9H4P9
20	75	20.4	68	6	Q95M68
21	74.5	20.3	79	11	Q8R215
22	74	20.2	69	11	Q8K4N2
23	73.5	20.0	65	13	Q9DG59
24	73	19.9	68	6	Q95M69
25	70	19.1	80	6	Q8SQD3
26	70	19.1	82	6	Q8SQCS
27	68.5	18.7	39	4	Q8NES9
28	68	18.5	68	6	Q95M66
29	67	18.3	68	6	Q95M67
30	67	18.3	68	6	Q95J22
31	66.5	18.1	63	11	Q8R213
32	66	18.0	68	6	Q95J24
33	66	18.0	68	11	Q8VBV2
34	66	18.0	919	13	Q8UVRO
35	66	18.0	936	13	Q8UVQ9
36	64.5	17.6	77	11	Q8R217
37	64	17.4	68	6	Q95J18
38	64	17.4	624	13	Q8DEQ0
39	63.5	17.3	1593	13	Q8JHV8
40	63	17.2	329	4	Q96S04
41	62.5	17.0	565	2	Q9F3S8
42	62	16.9	50	6	Q8WNZ3
43	62	16.9	4578	13	Q42181
44	61.5	16.8	77	4	Q8IZN8
45	61.5	16.8	78	4	Q8NG35

## ALIGNMENTS

### RESULT 1

Q8NFG6 PRELIMINARY; PRT; 67 AA.  
AC Q8NFG6; PRELIMINARY; PRT; 67 AA.  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)  
DE Beta-defensin-3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tonsil;  
RA Chen S., He F., Li R.;  
RT "Cloning and expression of Chinese human beta defensin-3."  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF516673; AAM62424.1; -  
SQ SEQUENCE 67 AA; 7750 MW; 15266DE1C90D5709 CRC64;

Query Match 96.7%; Score 355; DB 4; Length 67;

Best Local Similarity 98.5%; Pred No. 4.9e-38;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVLPVPGHGIIINTLQKYCYVRGGRCAVLSCLPKEQIGKSTRG 60

Db 1 MRIHYLLFALLFLVLPVPGHGIIINTLQKYCYVRGGRCAVLSCLPKEQIGKSTRG 60

QY 61 KCCRKK 67

Db 61 KCCRKK 67

### RESULT 2

Q95JD2 PRELIMINARY; PRT; 64 AA.

ID Q95JD2

AC Q95JD2;

DT 01-DEC-2001 (Tremblrel. 19, Created)

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DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Beta-defensin-3 (Fragment).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Duit L.A., Langermans J.A.M., Ravensbergen B., Paltensing S.,
RA Vervenne R.A.W., Hiemstra P.S., Thomas A.W., Nibbering P.H.;
RT "Expression of chimpanzee (Pan troglodytes) beta-defensin-3";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY033893; AAK61549.1; -.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
FT NON TER 64
SQ SEQUENCE 64 AA; 7299 MW; 01C90D4860218DC8 CRC64;

Query Match 95.1%; Score 349; DB 6; Length 64;
Best Local Similarity 98.4%; Pred. No. 2.7e-37;
Matches 63; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRHYLLFALLFLVLPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKCTRGR 60
Db |||||
QY 61 KCCR 64
Db |||||
QY 61 KCCR 64

RESULT 3
Q9TT12 PRELIMINARY; PRT; 64 AA.
AC Q9TT12;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Beta-defensin-2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Duit L.A., Langermans J.A.M., van der Straaten T., Vervenne R.A.W.,
RA Paltensing S., Prost P.A., Hiemstra P.S., Thomas A.W., Nibbering P.H.;
RT "Expression of beta-defensin-2 in chimpanzee (Pan troglodytes).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF209855; AAF20154.1; -.
DR HSSP; O15263; IPD3.
DR InterPro; IPR001855; Defensin_beta.
DR InterPro; IPR006080; Defensin_mammal.
DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00048; DEFSN; 1.
SQ SEQUENCE 64 AA; 7068 MW; B0D2454CE7ACCD13 CRC64;

Query Match 36.8%; Score 135; DB 6; Length 64;
Best Local Similarity 42.4%; Pred. No. 8.2e-10;
Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

QY 1 MRHYLLFALLFLVLPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKCTRGR 59
Db |||||
QY 60 RKCCR 65
Db |||||
QY 58 TKCCR 63

RESULT 4
Q9TT12 PRELIMINARY; PRT; 64 AA.
AC Q9TT12;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Beta-defensin-2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Duit L.A., Langermans J.A.M., van der Straaten T., Vervenne R.A.W.,
RA Paltensing S., Prost P.A., Hiemstra P.S., Thomas A.W., Nibbering P.H.;
RT "Expression of beta-defensin-2 in chimpanzee (Pan troglodytes).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF209855; AAF20154.1; -.
DR HSSP; O15263; IPD3.
DR InterPro; IPR001855; Defensin_beta.
DR InterPro; IPR006080; Defensin_mammal.
DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00048; DEFSN; 1.
SQ SEQUENCE 64 AA; 7068 MW; B0D2454CE7ACCD13 CRC64;

Query Match 36.8%; Score 135; DB 6; Length 64;
Best Local Similarity 42.4%; Pred. No. 8.2e-10;
Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

QY 1 MRHYLLFALLFLVLPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKCTRGR 59
Db |||||
QY 60 RKCCR 65
Db |||||
QY 58 TKCCR 63

RESULT 5
Q97942 PRELIMINARY; PRT; 64 AA.
AC Q97942;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Beta-defensin-2 precursor.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20002622; PubMed=10531296;
RA Zhao C., Nguyen T., Liu L., Shamova O., Brogden K., Lehrer R.I.;
RT "Differential expression of caprine beta-defensins in digestive and
RT respiratory tissues";
RL Infect. Immun. 67:6221-6224 (1999).
DR EMBL; AJ009877; CAA08905.1; -.
DR HSSP; P46170; 1BNB.
DR InterPro; IPR001855; Defensin_beta.
DR InterPro; IPR006080; Defensin_mammal.
DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00048; DEFSN; 1.
KW Signal.
FT CHAIN 1 26 POTENTIAL.
FT CHAIN 27 64 BETA DEFENSIN-2.
SQ SEQUENCE 64 AA; 7165 MW; 8672F5D9BFP800BA CRC64;

Query Match 28.6%; Score 105; DB 6; Length 64;
Best Local Similarity 43.3%; Pred. No. 5.9e-06;

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Q9BDS9 PRELIMINARY; PRT; 64 AA.
ID Q9BDS9;
AC Q9BDS9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Beta-defensin 2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21137962; PubMed=11238224;
RA Bals R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;
RT "Rhesus Monkey (Macaca mulatta) Mucosal Antimicrobial Peptides Are
RT Close Homologues of Human Molecules.";
RL Clin. Diagn. Lab. Immunol. 8:370-375 (2001).
DR EMBL; AF288286; AAK26259.1; -.
DR HSSP; O15263; IPD3.
DR InterPro; IPR001855; Defensin_beta.
DR InterPro; IPR006080; Defensin_mammal.
DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00048; DEFSN; 1.
DR DR SMART; SM00048; DEFSN; 1.
SQ SEQUENCE 64 AA; 7065 MW; BB26454CE7ACDDDF CRC64;

Query Match 36.5%; Score 134; DB 6; Length 64;
Best Local Similarity 42.4%; Pred. No. 1.1e-09;
Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

QY 1 MRHYLLFALLFLVLPVPGHGGIINTLQKYCYVRGRCVAVLSCLPKKEQIGKCTRGR 59
Db |||||
QY 1 MRVYLLFSLFIFLPLPGVFGIGDPVT---CLKNGAICHVPFCPRRYKQIGTGLPG 57
QY 60 RKCCR 65
Db |||||
QY 58 TKCCR 63

RESULT 5
Q97942 PRELIMINARY; PRT; 64 AA.
ID Q97942;
AC Q97942;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Beta-defensin-2 precursor.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20002622; PubMed=10531296;
RA Zhao C., Nguyen T., Liu L., Shamova O., Brogden K., Lehrer R.I.;
RT "Differential expression of caprine beta-defensins in digestive and
RT respiratory tissues";
RL Infect. Immun. 67:6221-6224 (1999).
DR EMBL; AJ009877; CAA08905.1; -.
DR HSSP; P46170; 1BNB.
DR InterPro; IPR001855; Defensin_beta.
DR InterPro; IPR006080; Defensin_mammal.
DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00048; DEFSN; 1.
KW Signal.
FT CHAIN 1 26 POTENTIAL.
FT CHAIN 27 64 BETA DEFENSIN-2.
SQ SEQUENCE 64 AA; 7165 MW; 8672F5D9BFP800BA CRC64;

Query Match 28.6%; Score 105; DB 6; Length 64;
Best Local Similarity 43.3%; Pred. No. 5.9e-06;

```

Matches 29; Conservative 3; Mismatches 31; Indels 4; Gaps 2;

QY 1 MRHYLLPALLFLVPVPGH-GGIINTLQKYCRVGRGCAVLSCLPKEQIGKSTRG 59  
 DB 1 MRHLHLLALFLVLGAGSGTGGIINHRG---CYRNKGVCAPARPNRQIGTCHGPP 57

QY 60 KRCRRK 66  
 DB 58 VKCRRK 64

RESULT 6

Q9PWF3 ID Q9PWF3 PRELIMINARY; PRT; 65 AA.

AC Q9PWF3; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Crotamine isoform precursor.

GN CRO2 OR CRT-P1.

OS Crotalus durissus terrificus (South American rattlesnake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Crotalus.

OC NCBI\_TaxID=8732;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RX MEDLINE=99314847; PubMed=10484745;

RA Radi-Baptista G., Oguiura N., Hayashi M.A.F., Camargo M.E., Grego K., Brandt E.P., Yamane T.;

RT "Nucleotide sequence of crotamine isoform precursors from a single South American rattlesnake (Crotalus durissus terrificus).";

RL Toxicon 37:973-984(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=9706, and 9705; TISSUE=Liver;

RA Radi-Baptista G., Oguiura N., Penteado-Rodrigues J., Yamane T.;

RT "Structural organization of crotamine genes encoding a myotoxin in the venom of South American rattlesnake (Crotalus durissus terrificus).";

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF053075; AAC06241.1; -

DR EMBL; AF223947; AAF34911.1; -

DR EMBL; AF223946; AAF34910.1; -

DR InterPro; IPR000881; Myotoxin.

DR Pfam; PF00819; Myotoxins; 1.

DR PRINTS; PR00283; MYOTOXIN.

DR ProDom; PD005972; Myotoxin; 1.

DR PROSITE; PS00459; MYOTOXINS; 1.

KW Signal.

FT SIGNAL

FT CHAIN

SQ SEQUENCE 65 AA; 7519 MW; FD109153C5BCCE33 CRC64;

Query Match 28.6%; Score 105; DB 13; Length 65;  
 Best Local Similarity 39.7%; Pred. No. 5.9e-06;  
 Matches 27; Conservative 7; Mismatches 24; Indels 10; Gaps 4;

QY 1 MRHYLLPALLFLVPVPGH-GGIINTLQKYCRVGRGCAVLSCLPKEQIGKSTR 58  
 DB 1 MKILYLLFAFLFLSEPG-----NAYKQ--CHKKGHCFFPKKICLPSSDFGKMDCR 53

QY 59 GR-KCCRR 65  
 DB 54 WRWKCKCK 61

RESULT 7

O57540 ID O57540 PRELIMINARY; PRT; 65 AA.

AC O57540; 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Crotamine precursor.

GN CRO1.

OS Crotalus durissus terrificus (South American rattlesnake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Crotalus.

OC NCBI\_TaxID=8732;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RX MEDLINE=99314847; PubMed=10484745;

RA Radi-Baptista G., Oguiura N., Hayashi M.A., Camargo M.E., Grego K.F., Oliveira E.B., Yamane T.;

RT "Nucleotide sequence of crotamine isoform precursors from a single South American rattlesnake (Crotalus durissus terrificus).";

RL Toxicon 37:973-984(1999).

DR EMBL; AF044674; AAC02995.1; -

DR InterPro; IPR000881; Myotoxin.

DR Pfam; PF00819; Myotoxins; 1.

DR PRINTS; PR00283; MYOTOXIN.

DR ProDom; PD005972; Myotoxin; 1.

DR PROSITE; PS00459; MYOTOXINS; 1.

KW Signal.

FT SIGNAL

FT CHAIN

SQ SEQUENCE 65 AA; 7519 MW; F840C453C5BCCE33 CRC64;

Query Match 28.1%; Score 103; DB 13; Length 65;  
 Best Local Similarity 38.2%; Pred. No. 1.1e-05;  
 Matches 26; Conservative 8; Mismatches 24; Indels 10; Gaps 4;

QY 1 MRHYLLPALLFLVPVPGH-GGIINTLQKYCRVGRGCAVLSCLPKEQIGKSTR 58  
 DB 1 MKILYLLFAFLFLSEPG-----NAYKQ--CHKKGHCFFPKKICLPSSDFGKMDCR 53

QY 59 GR-KCCRR 65  
 DB 54 WRWKCKCK 61

RESULT 8

Q91V70 ID Q91V70 PRELIMINARY; PRT; 71 AA.

AC Q91V70; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Beta-defensin 7 precursor.

GN DEFB7.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA Krause A.;

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA Conejo-Garcia J.R., Nehls M.C., Wattler S., Bales R., Heitland A., Kluever E., Liepke C., Adermann K., Forssmann W.G.;

RT "Cloning and characterization of mBD-7 and mBD-8, two novel mouse beta-defensins.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ298147; CAC44541.1; -

DR EMBL; AJ298148; CAC44542.1; -

DR MGD; MGI:2179200; Defb7.

KW Signal.

FT SIGNAL

FT CHAIN

SQ SEQUENCE 71 AA; 8292 MW; 8FB7A8A89146DF60 CRC64;

DR	EMBL; AB063109; BAB61108.1; -
MGD;	MGI:2151044; Defdb6.
SQ	SEQUENCE 63 AA; 6977 MW; 15PDAB06429D924E CRC64;
Query Match	26.8%; Score 98.5; DB 11; Length 63;
Best Local Similarity	37.9%; Pred. No. 3.9e-05;
Matches	25; Conservative 7; Mismatches 31; Indels 3; Gaps 2;
Qy	1 MRHYLLFALLFLVPVPGHGGIINTLQKYCRVRGRCVAVLSCLPKBEQIGKCSTRGR 60  :      : :  :
Db	1 MKTHYLLFAFILWMLPLAFAFSQLINS--PVTCMSYGGSQ-RSCNGGFRLLGGCHGHPKI 57  :      : :  :
Qy	61 KCCRRK 66 :
Db	58 RCCRK 63 :
RESULT 11	
Q9DG58	PRELIMINARY; PRT; 80 AA.
ID	Q9DG58
AC	Q9DG58;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE	Beta-defensin prepropeptide.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OX	NCBI_TaxID=9031;
XP	[1]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Trachea;
RC	MEDLINE=21153640; PubMed=11254635;
RX	Zhao C., Nguyen T., Liu L., Sacco R.E., Brogden K.A., Lehrer R.I.;
RT	"Gallacin-3, an Inducible Epithelial beta-Defensin in the Chicken.";
RL	Infect. Immun. 69:2684-2691(2001).
DR	EMBL; AF181952; AAC09212.1; -
DR	InterPro; IPR006080; Defensin_mammal.
DR	SMART; SM00048; DBFSN; 1.
SQ	SEQUENCE 80 AA; 8746 MW; 496BBC6BF3F5C3F CRC64;
Query Match	26.3%; Score 96.5; DB 13; Length 80;
Best Local Similarity	41.5%; Pred. No. 9e-05;
Matches	27; Conservative 2; Mismatches 27; Indels 9; Gaps 2;
Qy	1 MRHYLLFALLFLVPVPGHGGIINTLQKYCRVRGRCVAVLSCLPKBEQIGKCSTRGR 60   MRIVYLIPFFLFLOGAG-----TATQCRIIRGGFCRVGSCRPHIAIGKCAT-FI 51  :      :
Db	1 MRIVYLIPFFLFLOGAG-----TATQCRIIRGGFCRVGSCRPHIAIGKCAT-FI 51  :      :
Qy	61 KCCRR 65 
Db	52 SCCGR 56 
RESULT 12	
Q73799	PRELIMINARY; PRT; 64 AA.
ID	Q73799
AC	Q73799;
DT	01-AUG-1998 (TrEMBLrel. 07, Created)
DT	01-AUG-1998 (TrEMBLrel. 07, Last sequence update).
DE	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Crotamine.
GN	CHO3
OS	Eukalyurus durisus terrificus (South American rattlesnake).
OC	Karyozoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidodactylus; Squamata; Sceleroglossa; Serpentes; Colubroidea;
OC	Viperidae; Crocodylia; Crocodylinae; Crocodylidae;
OX	NCBI_TaxID=8732;
XP	[1]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Venom gland;
RC	MEDLINE=99314847; Pubmed=10484745;
RX	

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RA Radis-Baptista G., Oguira N., Hayaishi M.A., Camargo M.E., Grego K.F.,
RA Oliveira E.B., Yamane T.;
RT "Nucleotide sequence of crotamine isoform precursors from a single
RT South American rattlesnake (Crotalus durissus terrificus).";
RL Toxicon 37:973-984(1999).
DR EMBL; AF055988; AAC19036.1; -.
DR InterPro; IPR000881; Myotoxin.
DR Pfam; PF00819; Myotoxins; 1.
DR PRINTS; PR00283; MYOTOXIN.
DR ProDom; PD005972; Myotoxin; 1.
DR PROSITE; PS00459; MYOTOXINS; 1.
SQ SEQUENCE 64 AA; 7391 MW; 9B763190F34CCE35 CRC64;

Query Match 26.2%; Score 96; DB 13; Length 64;
Best Local Similarity 37.9%; Pred. No. 8.4e-05;
Matches 25; Conservative 7; Mismatches 24; Indels 10; Gaps 4;

QY 3 IHVLLFALLFLFVVPVGHGIIINTLQKYCRVGRGCAVLSCLPKEQIGKCTRGR 60
Db 2 ILVLLFALLFLFVVPVGHGIIINTLQKYCRVGRGCAVLSCLPKEQIGKCTRGR 60
QY 61 -KCCR 65
Db 55 WKCKK 60

RESULT 13
QY 08R556 PRELIMINARY; PRT; 60 AA.
AC Q8R556;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Defensin related peptide.
GN DEF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Morrison G.M.;
RT "Identification and characterisation of Defr1 : a novel murine beta
RT defensin related gene.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344114; CAC86998.1; -.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
SQ SEQUENCE 60 AA; 6820 MW; 3702A95649120351 CRC64;

Query Match 25.3%; Score 93; DB 11; Length 60;
Best Local Similarity 35.9%; Pred. No. 0.00019;
Matches 23; Conservative 7; Mismatches 30; Indels 4; Gaps 2;

QY 1 MRIHYLLFALLFLFVVPVGHGIIINTLQKYCRVGRGCAVLSCLPKEQIGKCTRGR 60
Db 1 MRIHYLLFTLLVLLSLPAAFSQKINDPVY---IRNGGICQYRCIGLRHKIGTCGS-PF 56
QY 61 KCCR 64
Db 57 KCCK 60

RESULT 14
QY 091V82 PRELIMINARY; PRT; 60 AA.
AC Q91V82;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Beta-defensin 8 (Beta-defensin 6).
GN DEF8.
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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Conejo-Garcia J.R., Nehls M.C., Wattler S., Bals R., Heitland A.,
RA Kluever E., Liepke C., Adermann K., Forgemann W.G.;
RT "Cloning and characterization of mBD-7 and mBD-8, two novel mouse
RT beta-defensins.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Krause A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ300674; CAC44635.1; -.
DR EMBL; AJ300673; CAC44634.1; -.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
SQ SEQUENCE 60 AA; 6760 MW; 7213024CF909A59B CRC64;

Query Match 25.1%; Score 92; DB 11; Length 60;
Best Local Similarity 37.5%; Pred. No. 0.00026;
Matches 24; Conservative 7; Mismatches 29; Indels 4; Gaps 3;

QY 1 MRIHYLLFALLFLFVVPVGHGIIINTLQKYCRVGRGCAVLSCLPKEQIGKCTRGR 60
Db 1 MRIHYLLFTLLVLLSLPAAFSQKIN--EPVSCIRNGGICQ-YRCIGLRHKIGTCGS-PF 56
QY 61 KCCR 64
Db 57 KCCK 60

RESULT 15
QY 09DG57 PRELIMINARY; PRT; 59 AA.
AC Q9DG57;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-defensin prepropeptide.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Trachea;
RX MEDLINE=21153640; PubMed=11254635;
RA Zhao C., Nguyen T., Liu L., Sacco R.E., Brogden K.A., Lehrer R.I.;
RT "Gallinacin-3, an Inducible Epithelial beta-Defensin in the Chicken.";
RL Infect. Immun. 69:2684-2691(2001).
DR EMBL; AF181953; AAG09213.1; -.
SQ SEQUENCE 59 AA; 6604 MW; 39F0CEB91AE3E35 CRC64;

Query Match 24.4%; Score 89.5; DB 13; Length 59;
Best Local Similarity 39.7%; Pred. No. 0.00053;
Matches 25; Conservative 2; Mismatches 27; Indels 9; Gaps 2;

QY 1 MRIHYLLFALLFLFVVPVGHGIIINTLQKYCRVGRGCAVLSCLPKEQIGKCTRGR 60
Db 1 MRIHYLLFPFFLLFQSAAG-----TPIQCRIRGGFCRFGSCRPPHAIKCAT-FI 51
QY 61 KCC 63
Db 52 PCC 54

Search completed: October 31, 2003, 14:03:44
Job time : 98 secs
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